

SEQUENCE LISTING

<110> Dumas Milne Edwards, Jean Baptiste
Bougueleret, Lydie
Jobert, Severin

<120> FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

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<150> US 09/731,872

<151> 2000-12-07

<150> US 60/187,470

<151> 2000-03-06

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His	Ser	Thr	Leu	Ser	Val	Asn	Trp	Ser	Leu	Leu	Leu	Ser	Pro	Glu	Pro	
		55				60					65					
gat	ggg	ggc	ctg	atg	gtg	ctc	cct	aag	gac	agc	att	cag	ttt	tct	tct	390
Asp	Gly	Gly	Leu	Met	Val	Leu	Pro	Lys	Asp	Ser	Ile	Gln	Phe	Ser	Ser	
70					75					80				85		
gcc	ctt	gtt	ttt	acc	agg	ctg	ctt	gag	ttt	gac	agc	acc	aac	gtg	tcc	438
Ala	Leu	Val	Phe	Thr	Arg	Leu	Leu	Glu	Phe	Asp	Ser	Thr	Asn	Val	Ser	
				90					95					100		
gat	acg	gca	gca	aag	cct	ttg	gga	aga	cca	tat	cct	cca	tac	tcc	ttg	486
Asp	Thr	Ala	Ala	Lys	Pro	Leu	Gly	Arg	Pro	Tyr	Pro	Pro	Tyr	Ser	Leu	
			105					110					115			
gcc	gat	ttc	tct	tgg	aac	aac	atc	act	gat	tca	ttg	gat	cct	gcc	acc	534
Ala	Asp	Phe	Ser	Trp	Asn	Asn	Ile	Thr	Asp	Ser	Leu	Asp	Pro	Ala	Thr	
		120					125					130				
ctg	agt	gcc	aca	ttt	caa	ggc	cac	ccc	atg	aac	gac	cct	acc	agg	act	582
Leu	Ser	Ala	Thr	Phe	Gln	Gly	His	Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr	
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ttt	gcc	aat	ggc	agc	ctg	gcc	ttc	agg	gtc	cag	gcc	ttt	tcc	agg	tcc	630
Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe	Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser	
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Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg	Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	
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cag	cta	gag	gtg	gcc	ctg	att	gga	gcc	tct	ccc	cgg	gga	aac	cgt	tcc	726
Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly	Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	
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Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	
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Ser	Met	Gln	Glu	Gln	His	Ser	Ile	Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	
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Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp	Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala	
230					235					240					245	
cag	tgg	cga	cca	gtg	gct	tac	tcc	cag	aag	ccg	ggg	ggc	cga	gaa	tca	918
Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser	Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	
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gcc	ctg	ccc	tgc	caa	gct	tcc	cct	ctt	cat	cct	gcc	tta	gca	tac	tct	966
Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro	Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	
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ctt	ccc	cag	tca	ccc	att	gtc	cga	gcc	ttc	ttt	ggg	tcc	cag	aat	aac	1014
Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg	Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	
		280					285					290				
ttc	tgt	gcc	ttc	aat	ctg	acg	ttc	ggg	gct	tcc	aca	ggc	cct	ggc	tat	1062
Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe	Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	

295	300	305	
tgg gac caa cac tac ctc agc tgg tgc atg ctc	ctg ggt gtg ggc ttc	1110	
Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu	Leu Gly Val Gly Phe		
310	315	320	325
cct cca gtg gac ggc ttg tcc cca cta gtc	ctg ggc atc atg gca gtg	1158	
Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu	Gly Ile Met Ala Val		
330	335	340	
gcc ctg ggt gcc cca ggg ctc atg	ctg cta ggg ggc ggc ttg gtt ctg	1206	
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly	Gly Gly Leu Val Leu		
345	350	355	
ctg ctg cac cac aag aag tac tca gag tac cag	tcc ata aat	1248	
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln	Ser Ile Asn		
360	365	370	
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aaaaaaaaa aaaaa		1623	

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 seq LGMLLGLLMAACT/PS

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Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala	
-15 -10 -5	
gcc tgc aca cct tct gcc tca gtc atc aga acc tgaaggagtt	tgccctgacc 163
Ala Cys Thr Pro Ser Ala Ser Val Ile Arg Thr	
1 5	
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ctggatgccg aagtcctgga ggtgttccac ccgacgcacg	agtggcaggc ccttcagcca 283
gggcaggctg tccctgcagg atcccacgta cggctgaatc	ttcagactgg ggaaagagag 343
gcaaaaactcc aatatgagga caagttccga aataatttga	aaggcaaaaag gctggatatc 403
aacaccaaca cctacacatc tcaggatctc aagagtgcac	tggcaaaatt caaggagggg 463
gcagagatgg agagttcaaa ggaagacaag gcaaggcagg	ctgaggtaaa gcggctcttc 523
cgccccattg aggaactgaa gaaagacttt gatgagctga	atgttgatc tgaagactgac 583
atgcagatca tggtagggct gatcaacaag ttcaatagtt	ccagctccag tttggaagag 643
aagattgctg cgctctttga tcttgaatat tatgtccatc	agatggacaa tgccgaggac 703
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ccgctcactg caaaggaggg tgctcaccgt gcgcgtggtc	acactgctct acgacctggt 943

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cacggagaag atgttcgccg aggaggagggc tgagctgacc caggagatgt ccccagagaa 1003
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                                     Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu
      -25                                -20                                -15
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac 212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
      -10                                -5                                1                                5
ctg aag gag ttt gcc ctg acc aac cca gag aag agc agc acc aaa gaa 260
Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
      10                                15                                20
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
      25                                30                                35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
      40                                45                                50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
      55                                60                                65
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg 452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
      70                                75                                80                                85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat 500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
      90                                95                                100
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
      105                                110                                115
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596

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Ser	Lys	Glu	Asp	Lys	Ala	Arg	Gln	Ala	Glu	Val	Lys	Arg	Leu	Phe	Arg	
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Pro	Ile	Glu	Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile	
	135					140					145					
gag	act	gac	atg	cag	atc	atg	gta	cgg	ctg	atc	aac	aag	ttc	aat	agt	692
Glu	Thr	Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser	
150					155					160					165	
tcc	agc	tcc	agt	ttg	gaa	gag	aag	att	gct	gcg	ctc	ttt	gat	ctt	gaa	740
Ser	Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu	
				170					175					180		
tat	tat	gtc	cat	cag	atg	gac	aat	gcg	cag	gac	ctg	ctt	tcc	ttt	ggg	788
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	Gly	
			185				190						195			
ggg	ctt	caa	gtg	gtg	atc	aat	ggg	ctg	aac	agc	aca	gag	ccc	ctc	gtg	836
Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	Leu	Val	
		200					205					210				
aag	gag	tat	gct	gcg	ttt	gtg	ctg	ggc	gct	gcc	ttt	tcc	agc	aac	ccc	884
Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	Ser	Asn	Pro	
	215					220				225						
aag	gtc	cag	gtg	gag	gcc	atc	gaa	ggg	gga	gcc	ctg	cag	aag	ctg	ctg	932
Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	Gln	Lys	Leu	Leu	
230					235					240				245		
gtc	atc	ctg	gcc	acg	gag	cag	ccg	ctc	act	gca	aag	aag	aag	gtc	ctg	980
Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	Lys	Lys	Lys	Val	Leu	
				250					255					260		
ttt	gca	ctg	tgc	tcc	ctg	ctg	cgc	cac	ttc	ccc	tat	gcc	cag	cgg	cag	1028
Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe	Pro	Tyr	Ala	Gln	Arg	Gln	
			265				270					275				
ttc	ctg	aag	ctc	ggg	ggg	ctg	cag	gtc	ctg	agg	acc	ctg	gtg	cag	gag	1076
Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu	Arg	Thr	Leu	Val	Gln	Glu	
		280					285					290				
aag	ggc	acg	gag	gtg	ctc	gcc	gtg	cgc	gtg	gtc	aca	ctg	ctc	tac	gac	1124
Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val	Val	Thr	Leu	Leu	Tyr	Asp	
	295					300				305						
ctg	gtc	acg	gag	aag	atg	ttc	gcc	gag	gag	taggctgagc	tgacccagga					1174
Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu							
310					315											
gatgtcccca	gagaagctgc	agcagtatcg	ccaggtacac	ctcctgccag	gcctgtggga											1234
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score 4.89555877630516

seq LLLLRLNDAALRA/LQ

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Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys	
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ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac	158
Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp	
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gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg	206
Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro	
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gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct	254
Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro	
15 20 25	
ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag	302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu	
30 35 40	
ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct	350
Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser	
45 50 55	
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Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile	
60 65 70 75	
att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga	446
Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly	
80 85 90	
cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca	494
His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr	
95 100 105	
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Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu	
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Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser	
125 130 135	
ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc	638
Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser	
140 145 150 155	
cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct	686
Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser	
160 165 170	
gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act	734
Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr	
175 180 185	
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Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser	
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Pro Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp	
205 210 215	
gag caa gaa gat gag gac atg gac ccc aga tta gaa cac agt tcc tca	878
Glu Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser	
220 225 230 235	

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ctc ctg caa tac agg gcc atc cac agt gca gaa cag caa cat gcc tat      974
Leu Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr
      255                      260                      265
gag cag gac ttt gag aca gat tat gct gaa tac cgc atc ctg cat gcc      1022
Glu Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala
      270                      275                      280
cgt gtt ggg act gca agc caa agg ttc ata gag ctg gga gca gag att      1070
Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile
      285                      290                      295
aaa aga gtt cgg cga gga act cca gaa tac aag gtc ctg gaa gac aag      1118
Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys
      300                      305                      310                      315
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Ile Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg
      320                      325                      330
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Glu Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile
      335                      340                      345
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Lys Gly Leu Ile Leu Glu Phe Glu Lys Asn Arg Gly Ser
      350                      355                      360
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cgtccagggtg gcagagcagc taggaacgca aggcctgaac ctggggccag acacctgct      180
ctcccgggcc atg gtc aac gac cct cca gta cct gcc tta ctg tgg gcc cag      231
      Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln
      -20                      -15                      -10
gag gtg ggc caa gtc ttg gca ggc cgt gcc cgc agg ctg ctg ctg cag      279

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Phe	Gly	Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	
10				15						20					25	
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Phe	Leu	Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	
				30					35						40	
ctc	agc	cct	gtg	cat	ttc	tac	tac	agg	acc	gac	tgt	gat	tcc	tcc	acc	423
Leu	Ser	Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	
			45					50					55			
acc	tca	ctc	tgc	tcc	ttc	cct	gtt	gcc	aat	gtc	tcg	ctg	act	aag	ggc	471
Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	
		60					65					70				
gga	cgt	gat	cgg	gtg	ctg	atg	tat	gga	cag	ccg	tat	cgt	gtt	acc	tta	519
Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	
		75				80					85					
gag	ctt	gag	ctg	cca	gag	tcc	cct	gtg	aat	caa	gat	ttg	ggc	atg	ttc	567
Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	
90				95						100					105	
ttg	gtc	acc	att	tcc	tgc	tac	acc	aga	ggc	ggc	cga	atc	atc	tcc	act	615
Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	
				110					115						120	
tct	tcg	cgt	tcg	gtg	atg	ctg	cat	tac	cgc	tca	gac	ctg	ctc	cag	atg	663
Ser	Ser	Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	
				125				130							135	
ctg	gac	aca	ctg	gtc	ttc	tct	agc	ctc	ctg	cta	ttt	ggc	ttt	gca	gag	711
Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	
		140					145					150				
cag	aag	cag	ctg	ctg	gag	gtg	gaa	ctc	tac	gca	gac	tat	aga	gag	aac	759
Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	
		155				160					165					
tcg	gtg	agt	gag	tac	gtg	ccg	acc	act	gga	gcg	atc	att	gag	atc	cac	807
Ser	Val	Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	
170				175						180					185	
agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	cgc	atc	cac	gcg	cac	855
Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	
				190					195					200		
ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	ccg	atg	acc	tgc	gcc	903
Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys		

[illegible]

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Ala Trp Leu Phe
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<212> DNA
<213> Homo sapiens

<220>
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<222> 84..299

<220>
<221> sig_peptide
<222> 84..134
<223> Von Heijne matrix
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seq GFVAALVAGGVAG/VS

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gccttgacga ggtctgagcg acc atg gac cgg ccg ggg ttc gtg gca gcg ctg 113
Met Asp Arg Pro Gly Phe Val Ala Ala Leu
-15 -10
gtg gct ggt ggg gta gca ggt gtt tct gtt gac ttg ata tta ttt cct 161
Val Ala Gly Gly Val Ala Gly Val Ser Val Asp Leu Ile Leu Phe Pro
-5 1 5
ctg gat acc att aaa acc agg ctg cag agt ccc caa gga ttt aat aag 209
Leu Asp Thr Ile Lys Thr Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys
10 15 20 25
gct ggt ggt ttt cat gga ata tat gct ggc gtt cct tct gct gct att 257
Ala Gly Gly Phe His Gly Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile
30 35 40
gga tcc ttt cct aat ggt tgc ctg cct gat tcg agt tcc atc 299
Gly Ser Phe Pro Asn Gly Cys Leu Pro Asp Ser Ser Ser Ile
45 50 55
tgaagtgggt aagcagaggg cacaggtatc tgcttctaca agaacatttc agattttctc 359
taacatctta tatgaagagg gtatccaagg gttgtatcga ggctataaaa gcacagtttt 419
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actctgaaca atttcctcag aacctcttaa taaataagtt tggtaatgct gagggcaggc 1079

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ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
ataaatgaac ctttattaaa gacacttcaa tgcaaaaaaa aaaaaaaaaa 1849

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<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 55..468

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<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
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      seq FTLLFLAAVAGA/LV

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Met
-15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc 105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
-10 -5 1
tat gct gaa gat gcc tcc tct gac tcg acg ggt gct gat cct gcc cag 153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
5 10 15
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa 201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
20 25 30
cca gct tca ccc cca gag aca acc aca aca gcc cag gag act tcg gcg 249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
35 40 45 50
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta 297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
55 60 65
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa 345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
70 75 80
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga 393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
85 90 95
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag 441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
100 105 110

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aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga      488
Lys Phe Ser Leu Leu Lys Pro Trp Ala
115                      120
tcattgggact taaagcctta aatacccttg tagcccagag ctattaaaac gaaagcatcc      548
aaaaaaaaaaaa aaaaaaaa      565

<210> 12
<211> 1663
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..475

<220>
<221> sig_peptide
<222> 152..244
<223> Von Heijne matrix
      score 10.0910253445132
      seq LVLVVTRSPVNA/CL

<400> 12
atgtgtctgc tgccgccatt gtgcggcgct ggtccctca gagggttcct gctgctgccg      60
gtgccttgga cctcccccct cgcttctcgt tctactgcc caggagcccg gcgggtccgg      120
gactcccgtc cgtgccggtg cgggcgcggg c atg tgg ctg tgg gag gac cag      172
                               Met Trp Leu Trp Glu Asp Gln
                               -30          -25

ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg      220
Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu
                               -20          -15          -10

gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc      268
Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe
                               -5          1          5

gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc      316
Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala
10          15          20

ctg cag gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt      364
Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg
25          30          35          40

ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att cgg cag      412
Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln
45          50          55

cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg      460
Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu
60          65          70

acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgatgggac      515
Thr Gly Phe Leu Ser
75

tgggcgattg tgtgatttga catttgaaca aattaggaag ctgaatcctg cagcaaacca      575
cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaaggggaag ctgttgacga      635
gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac      695
tgaggctcta aagaaaatgt atatggaatt tcttcaactg tataataata gtgtgggtctg      755
ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag      815
atgagacaaa cagatcggga tgtaataaca gcattaactc acagaccttg gagcctaagc      875
catacaggag atgggaaacc acgctatgat actttctgga aacattttat atttgttatg      935
atggacattt tgctcgattg gagcatgcat aatatcttgt ggtacctgtg tggaatttca      995
gctttcctca tgcaaaaagga ttttgtatcc cgggcctact tgaagaagtg gtcagctaaa      1055

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ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc 1115
catcttggtt ccagctatat cactgacagc atggtagaag actgcgaacc tcacttctag 1175
actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatalc agggatatca 1235
aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
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gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcattgataa ctcagagttg 1535
acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt taacatgtac 1595
tgtagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
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<210> 13
<211> 744
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 112..552

<220>
<221> sig_peptide
<222> 112..183
<223> Von Heijne matrix
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<400> 13
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actgccagat ttttgtaaga ttcttctctc tgggagcctg tgttggaaga g atg gtg 117
                                     Met Val
atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
      -20                      -15                      -10
acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
      -5                      1                      5                      10
acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
      15                      20                      25
gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
      30                      35                      40
aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
      45                      50                      55
aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
      60                      65                      70
tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
      75                      80                      85                      90
cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
      95                      100                      105
tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg

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110      115      120
ccg taaccagcgg gcccttggtc aagtgtgtggc tctgtgtgcc ttgccttcca 602
Pro
tttccccctct gcaccagaaa cagtgggtggc aacattcatt gccaaagggcc caaagaaaaga 662
gctacctgga cctttttgttt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaaa aaaaaaaaaa aa 744

<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 101..1243

<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
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      seq FLCLGMALCPRQA/TR

<400> 14
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ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115
                        Met Ser Trp Thr Val
                        -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
      -25      -20      -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
      -10      -5      1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5      10      15      20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25      30      35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40      45      50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
      55      60      65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
      70      75      80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
      85      90      95      100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
      105      110      115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
      120      125      130

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ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa	643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys	
135 140 145	
ctg att att gtt tcc aat cca gtg gat atc tta act tat gta gct tgg	691
Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu Thr Tyr Val Ala Trp	
150 155 160	
aag ttg agt gca ttt ccc aaa aac cgt att att gga agc ggc tgt aat	739
Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile Gly Ser Gly Cys Asn	
165 170 175 180	
ctg gat act gct cgt ttt cgt ttc ttg att gga caa aag ctt ggt atc	787
Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly Gln Lys Leu Gly Ile	
185 190 195	
cat tct gaa agc tgc cat gga tgg atc ctc gga gag cat gga gac tca	835
His Ser Glu Ser Cys His Gly Trp Ile Leu Gly Glu His Gly Asp Ser	
200 205 210	
agt gtt cct gtg tgg agt gga gtg aac ata gct ggt gtc cct ttg aag	883
Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala Gly Val Pro Leu Lys	
215 220 225	
gat ctg aac tct gat ata gga act gat aaa gat cct gag caa tgg aaa	931
Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp Pro Glu Gln Trp Lys	
230 235 240	
aat gtc cac aaa gaa gtg act gca act gcc tat gag att att aaa atg	979
Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr Glu Ile Ile Lys Met	
245 250 255 260	
aaa ggt tat act tct tgg gcc att ggc cta tct gtg gcc gat tta aca	1027
Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val Ala Asp Leu Thr	
265 270 275	
gaa agt att ttg aag aat ctt agg aga ata cat cca gtt tcc acc ata	1075
Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His Pro Val Ser Thr Ile	
280 285 290	
att aag ggc ctc tat gga ata gat gaa gaa gta ttc ctc agt att cct	1123
Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val Phe Leu Ser Ile Pro	
295 300 305	
tgt atc ctg gga gag aac ggt att acc aac ctt ata aag ata aag ctg	1171
Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu Ile Lys Ile Lys Leu	
310 315 320	
acc cct gaa gaa gag gcc cat ctg aaa aaa agt gca aaa aca ctc tgg	1219
Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser Ala Lys Thr Leu Trp	
325 330 335 340	
gaa att cag aat aag ctt aag ctt taaagttgcc taaaactacc attccgaat	1273
Glu Ile Gln Asn Lys Leu Lys Leu	
345	
tattgaagag atcatagata caggattata taacgaaatt ttgaataaac ttgaattcct	1333
aaaagatgga aacaggaaag taggtagagt gattttccta tttatttagt cctccagctc	1393
ttttattgag catccacgtg ctggacgata cttattttaca attcctaagt attttttgta	1453
cctctgatgt agcagcactt gccatgttat atatattgtat ttggcatttg gttcccaaaa	1513
agtaggatgt aggtatttat tgtgttctag aaattccgac tcttttcatt agatatatgc	1573
tatttctttc attcttgctg gttttataacct atgtttcattt atatgctgta aaaaagtagt	1633
agcttcttct acaatgtaaa aataaatgta catacaaaaa aatgcagtag tatatacaat	1693
cttttgtttt gcttcctttg atagttaata aattccgttt gttgaatcaa taataaaaaa	1753
aaaaaa	1759

<210> 15

<211> 1755

<212> DNA

<213> Homo sapiens

<220>

<221> CDS
<222> 101..517

<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
score 3.57613483592743
seq FLCLGMALCLRQA/TR

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Met Ser Trp Thr Val
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cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe
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Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro
-10 -5 1
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Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5 10 15 20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
25 30 35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
40 45 50
atc agc atc ttg tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
55 60 65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70 75 80
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg 499
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
85 90 95 100
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Ser Gln Gln Thr Pro Thr
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gtagctttctt ctacaatgta aaaataaatg tacatacaaa aaaatgcagt agtatataca 1687
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Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
      -10      -5      1
agt agc act ttg aag cct act att gaa gca ttg cct aat gtg cta cct 154
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
      5      10      15
tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act 202
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
      20      25      30
ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat 250
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
      35      40      45      50
ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct 298
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
      55      60      65
gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
      70      75      80
gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
      85      90      95
ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac 442
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
      100      105      110
cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
      115      120      125      130
gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg 538
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
      135      140      145
acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg 586
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
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tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct 634

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Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly		
		180					185				190						
gtt	tca	gat	aca	tcc	ttt	tcc	aag	agt	gca	gag	agc	agc	aca	ttt	ttg	730	
Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu		
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ggg	acc	act	tct	tca	gat	atg	aga	aga	tca	ggc	aca	aga	aca	tca	gaa	778	
Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu		
				215					220					225			
tct	aag	ata	atg	acg	gat	atc	att	tcc	ata	ggc	tca	gat	aat	gag	atg	826	
Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met		
			230					235					240				
cat	gaa	aac	gat	gag	tcg	gtt	acc	cgg	tgaagaaatc	aaggaacccg						873	
His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg									
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	Met Asp Ser	Ser Thr Ala	His Ser Pro	Val Phe Leu	Val												
	-20		-15		-10												
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Phe Pro Pro	Glu Ile Thr	Ala Ser Glu	Tyr Glu Ser	Thr Glu	Leu Ser												
	-5		1		5												
gcc acg acc	ttt tca act	caa agc ccc	ttg caa aaa	tta ttt	gct aga											207	
Ala Thr Thr	Phe Ser Thr	Gln Ser Pro	Leu Gln Lys	Leu Phe	Ala Arg												
10		15		20	25												
aaa atg aaa	atc tta ggg	act atc cag	atc ctg ttt	gga att	atg acc											255	
Lys Met Lys	Ile Leu Gly	Thr Ile Gln	Ile Leu Phe	Gly Ile	Met Thr												
	30		35		40												
ttt tct ttt	gga gtt atc	ttc ctt ttc	act ttg tta	aaa cca	tat cca											303	
Phe Ser Phe	Gly Val Ile	Phe Leu Phe	Thr Leu Leu	Lys Pro	Tyr Pro												
	45		50		55												
agg ttt ccc	ttt ata ttt	ctt tca gga	tat cca ttc	tgg ggc	tct gtt											351	
Arg Phe Pro	Phe Ile Phe	Leu Ser Gly	Tyr Pro Phe	Trp Gly	Ser Val												
	60		65		70												
ttg ttc att	aat tct gga	gcc ttc cta	att gca gtg	aaa aga	aaa acc											399	
Leu Phe Ile	Asn Ser Gly	Ala Phe Leu	Ile Ala Val	Lys Arg	Lys Thr												

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Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
90              95              100              105
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta      495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
      110              115              120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag      543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
      125              130              135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc      591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
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agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc      639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
      155              160              165
cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata      692
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170              175              180
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      Met Ala Thr Ala Gln Leu Gln
      -35
agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa      162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
      -30              -25              -20
cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc      210
His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
      -15              -10              -5
tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca      258
Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
1              5              10              15
aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat      306
Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
      20              25              30
tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat      354
Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp
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gct tta cag aaa aaa tat cta agg atg gtt gtt cta gct gta tac aca      402

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Asn	Pro	Glu	Asp	Pro	Gln	Thr	Ile	Ser	Glu	Cys	Tyr	Gln	Phe	Lys	Phe	
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Lys	Tyr	Thr	Asn	Asn	Gly	Pro	Leu	Met	Asp	Phe	Ile	Ser	Lys	Asn	Gln	
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Ser	Asn	Glu	Ser	Ser	Met	Leu	Ser	Thr	Asp	Thr	Lys	Lys	Ala	Ser	Ile	
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ctc	ctc	att	cgc	aag	att	tat	atc	cta	atg	caa	aat	ctg	ggg	cct	tta	594
Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile	Leu	Met	Gln	Asn	Leu	Gly	Pro	Leu	
			115				120					125				
cct	aat	gat	gtt	tgt	ttg	acc	atg	aaa	ctt	ttt	tac	tat	gat	gaa	gtt	642
Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys	Leu	Phe	Tyr	Tyr	Asp	Glu	Val	
	130					135					140					
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Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly	Phe	Lys	Asp	Gly	Asp	Cys	Glu	
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Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp	Lys	Asp	Val	Glu	Asp	Glu	Gln	
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Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp	Ile	Glu	Thr	Lys	Met	Glu	Glu	
					230					235					240	
cag	gaa	aaa	aac	cct	gca	tct	tct	gaa	ctt	gaa	gaa	cca	agt	tta	gtt	978
Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu	Leu	Glu	Glu	Pro	Ser	Leu	Val	
				245					250					255		
tgt	gag	gaa	gat	gaa	att	atg	agg	tct	aaa	gaa	agt	cca	gat	ctt	tct	1026
Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser	Lys	Glu	Ser	Pro	Asp	Leu	Ser	
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Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu	Val	Asn	Lys	Thr	Ser	Glu	Leu	
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Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser	Gly	Lys	Val	Phe	Gln	Asn	Lys	
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Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys	Ser	Ser	Lys	Glu	Asn	Arg	Lys	
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Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile	Val	Leu	His	His	Phe	Asp	Ser	
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Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg	Arg	Lys	Phe	Ser	Glu	Pro	Lys	
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Glu	His	Ile														

355
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Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
-10 -5 1
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Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
5 10 15 20
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Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
25 30 35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
40 45 50
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
55 60 65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
70 75 80
gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
85 90 95 100
tca gtg tgg ctt aca cca gtt tct act gag aat gaa ata aaa ttg gat 440
Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
105 110 115
cct agt cct ttt att gct gac ttt cag aca aca gca gaa gag tta gga 488
Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly

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120      125      130
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Leu Leu Ser Ser Ser Pro Asn Leu Leu

135      140
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tctgaggggt acaggactta ccccagtggt aagcagctaa gcaggtctga ccagccgacc      240
tggacctggc caagggtcct gtcacccctc atg gcc acc ccg cca ttc cgg ctg      294
                                Met Ala Thr Pro Pro Phe Arg Leu
                                -30                                -25
ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc      342
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala
                                -20                                -15                                -10
tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa      390
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys
                                -5                                1                                5
cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa      438
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys
                                10                                15                                20
att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc      486
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe
25                                30                                35                                40
cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa      534
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu
                                45                                50                                55
gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa      582
Glu Glu Arg Pro Phe Trp Glu Glu Glu Lys Thr Phe Trp Lys Glu Glu
                                60                                65                                70
aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act      630
Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr
                                75                                80                                85

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ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg      678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp
90 95 100
aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105 110 115 120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
125 130 135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
140 145 150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
155 160 165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
170 175 180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185 190 195 200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccagggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcctgaggca aggtttggaa aaccaaaaaa aaaaaaaaaa      1138

<210> 21
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..276

<220>
<221> sig_peptide
<222> 76..135
<223> Von Heijne matrix
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      seq SPVFLVFPPEITA/SE

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atcaccgaca ccatac atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
      -20 -15 -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
      -5 1 5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
10 15 20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
25 30 35 40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser

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45
ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc 366
ctttctcaat tttgggggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag 426
cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa 468

<210> 22
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..287

<220>
<221> sig_peptide
<222> 6..80
<223> Von Heijne matrix
score 4.17710408129886
seq ISLSHLFLDLRS/LW

<400> 22
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu
-25 -20 -15
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys
-10 -5 1 5
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu
10 15 20
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val
25 30 35
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu
40 45 50
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
55 60 65
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa 347
atagtaagta aaatcttgct tgcctctcag taaaataaag ctctattttt cgtttttttt 407
ttttccaact tctgtacaa aaaagggaaa acttttagctt ttgggggaaa tttggagcta 467
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527
aatactttat aaagataattt tcataaatta cagcaatcct ggcttttagat gattgatggc 587
cattttttaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647
gtttcttaga aagtctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707
aaaaaaaaaa aaa 720

<210> 23
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..692

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<220>
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<222> 171..227
<223> Von Heijne matrix
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      seq LLLGQRCSLKVSG/QE

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tgggactact agccctttgt tgatagggag aagccaacat ctcccgcagg accccctaat      120
cttcagggca gctcccagag catggatccc tcctgattcc actcagcccg atg ttc      176
                               Met Phe
ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca      224
Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val Ser
      -15                               -10                               -5
ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg      272
Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
      1                               5                               10                               15
aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg      320
Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
      20                               25                               30
gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct      368
Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
      35                               40                               45
atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc      416
Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
      50                               55                               60
cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta      464
His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
      65                               70                               75
gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta      512
Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
      80                               85                               90                               95
agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg      560
Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu
      100                               105                               110
gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca      608
Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
      115                               120                               125
gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt      656
Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
      130                               135                               140
gac atg gag gag aag gag gag gca gca gct gat cag taaacggggcc      702
Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
      145                               150                               155
atcctaccgg aaaaaaaaaa aaaaaa      727

<210> 24
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 137..454

<220>
<221> sig_peptide

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<222> 137..187

<223> Von Heijne matrix

score 10.7019149919754

seq VLMLLAVLIWTGA/EN

<400> 24

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aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc      120
tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg      172
          Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
                    -15                      -10
att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg      220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5                      1                      5                      10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg      268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
          15                      20                      25
tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat      316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
          30                      35                      40
cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt      364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
          45                      50                      55
ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc      412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
60                      65                      70                      75
atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt      454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
          80                      85
taaaaaaaaaa aaaaaa      470

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<210> 25

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 238..609

<220>

<221> sig_peptide

<222> 238..291

<223> Von Heijne matrix

score 10.0374888212272

seq LLLLVMALPPGTT/GV

<400> 25

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attccattca cagactcttg ttgggcagca gccacccgct cacctccatc cccaggactt      60
agagggacgc agggcggttg gaacagagga cactccaggc gctgaccctg ggaggccagg      120
accagggcca aagtcccgct ggcaagagga gtcctcagag gtccttcatt cagcggttcc      180
gggaggtctg ggaagcccac ggcttggtg gggcagggtc aacgccgccca ggccgcc      237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc      285
Met Val Leu Cys Trp Leu Leu Leu Val Met Ala Leu Pro Pro Gly
          -15                      -10                      -5
acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg      333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
          1                      5                      10

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cag	tgt	cct	ggt	acc	tac	atg	cac	tgt	ggc	gat	gac	gag	gac	tgc	ttc		381
Gln	Cys	Pro	Gly	Thr	Tyr	Met	His	Cys	Gly	Asp	Asp	Glu	Asp	Cys	Phe		
15					20					25					30		
aca	ggc	cac	ggg	gtc	gcc	ccg	ggc	act	ggc	ccg	gtc	atc	aac	aaa	ggc		429
Thr	Gly	His	Gly	Val	Ala	Pro	Gly	Thr	Gly	Pro	Val	Ile	Asn	Lys	Gly		
				35					40					45			
tgc	ctg	cga	gcc	acc	agc	tgc	ggc	ctt	gag	gaa	ccc	gtc	agc	tac	agg		477
Cys	Leu	Arg		Thr	Ser	Cys	Gly	Leu	Glu	Glu	Pro	Val	Ser	Tyr	Arg		
				50				55						60			
ggc	gtc	acc	tac	agc	ctc	acc	acc	aac	tgc	tgc	acc	ggc	cgc	ctg	tgt		525
Gly	Val	Thr	Tyr	Ser	Leu	Thr	Thr	Asn	Cys	Cys	Thr	Gly	Arg	Leu	Cys		
				65				70					75				
aac	aga	gcc	ccg	agc	agc	cag	aca	gtg	ggg	gcc	acc	acc	agc	ctg	gca		573
Asn	Arg	Ala	Pro	Ser	Ser	Gln	Thr	Val	Gly	Ala	Thr	Thr	Ser	Leu	Ala		
				80				85					90				
ctg	ggg	ctg	ggt	atg	ctg	ctt	cct	cca	cgt	ttg	ctg	tgaccaacag					619
Leu	Gly	Leu	Gly	Met	Leu	Leu	Pro	Pro	Arg	Leu	Leu						
95					100					105							
ggaggacagg	gcctgggact			gttctccccag			atccgccact			ccccatgtcc			ccatgtcctt				679
ccccactaa	atggccagag			agGCCctgga			caacctcttg			cgGCCctggc			ttcatccctt				739
ctaaggctgt	ccaccaggag			ccCGgtgcta			ggggGagcat			cccCaggcct			gactgagcgg				799
caggggagca	cggCCCgtgg			gtttgattgt			attactctgt			tcCactgggt			ctaagacgca				859
gagcttctca	catctcaatc			aggatgcttc			tctccattgg			tagCacttta			gagtccatga				919
aaatatgtaa	aaaatatata			tatatcataa			taaaatgacag			ctgatgttca			tggaaaaaaa				979
aaaaaaaa																	987

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<210> 26
<211> 908
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 80..862
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<220>
<221> sig_peptide
<222> 80..127
<223> Von Heijne matrix
      score 3.66725851505537
      seq FSLLSISGPPIS/SA
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<400> 26																
gaatgtttat cctctggaca aaccagccag cctctccaga gcaggcgtgt gatctctgta																60
ccccgcagtg ggtcagaat atg gag aac ttc tca ctc ctc agc atc tct gga																112
Met Glu Asn Phe Ser Leu Leu Ser Ile Ser Gly																
-15 -10																
cct cca atc tct tcc tcc gcc ctg agt gct ttt ccc gac att atg ttc																160
Pro Pro Ile Ser Ser Ser Ala Leu Ser Ala Phe Pro Asp Ile Met Phe																
-5 1 5 10																
tct cgt gcc acc agc ctg cca gac att gca aag aca gca gta ccc act																208
Ser Arg Ala Thr Ser Leu Pro Asp Ile Ala Lys Thr Ala Val Pro Thr																
15 20 25																
gag gca tcc agc cca gct cag gcc ctg cca ccc cag tac caa agc atc																256
Glu Ala Ser Ser Pro Ala Gln Ala Leu Pro Pro Gln Tyr Gln Ser Ile																
30 35 40																
att gtc agg caa ggg ata cag aac aca gtg ctc tca cca gac tgc agc																304
Ile Val Arg Gln Gly Ile Gln Asn Thr Val Leu Ser Pro Asp Cys Ser																

45	50	55	
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc			352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile			
60	65	70	75
tac cgg ccc tgg ttc tcc ccc tac agc tac ttc gtg tgt gca gac aaa			400
Tyr Arg Pro Trp Phe Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys			
80	85	90	
gag agc cag ctg gag gcc tat gac ttc cca gag gtg cag cag gat gag			448
Glu Ser Gln Leu Glu Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu			
95	100	105	
ggc aag tgg gac aac tgc ctt tct gag gac atg gct gag aac atc tgt			496
Gly Lys Trp Asp Asn Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys			
110	115	120	
tcg tcc tct tcc tcc cca gag aac act tgc cct cga gaa gcc acc aag			544
Ser Ser Ser Ser Ser Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys			
125	130	135	
aaa tcc agg cat ggc ctg gac tcc atc aca tcc cag gac atc cta atg			592
Lys Ser Arg His Gly Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met			
140	145	150	155
gct tcc aga tgg cac cca gca cag cag aat ggc tac aag tgc gtg gcc			640
Ala Ser Arg Trp His Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala			
160	165	170	
tgc tgc cgc atg tac ccc acc ctg gac ttc ctc aag agc cac atc aag			688
Cys Cys Arg Met Tyr Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys			
175	180	185	
agg ggc ttc agg gag ggc ttc agc tgc aag gtg tac tac cgc aag ctc			736
Arg Gly Phe Arg Glu Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu			
190	195	200	
aaa gcc ctc tgg agc aag gag cag aag gcc cgg ctg gga gac agg ctc			784
Lys Ala Leu Trp Ser Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu			
205	210	215	
tcc tcc ggc agc tgc cag gcc ttc aat agt cct gct gaa cac ctt agg			832
Ser Ser Gly Ser Cys Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg			
220	225	230	235
caa att ggc ggt gaa gcc tac tta tgt ctc tagagagatg ccaataaagt			882
Gln Ile Gly Gly Glu Ala Tyr Leu Cys Leu			
240	245		
tagtcacagc caaaaaaaaa aaaaaa			908

<210> 27
 <211> 762
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..310

<220>
 <221> sig_peptide
 <222> 83..157
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 score 4.72955689475746
 seq LCALLSNFCPSTT/VK

<400> 27	
ttttttctac tacaaacgcc atgggggatgc ggggtctggga acagcggaaa accctaccct	60
gccctgaaaa gtccttggt ca atg tgc atg tcc ctt tct atg aaa gtt cct	112

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Met Cys Met Ser Leu Ser Met Lys Val Pro
-25 -20
tgc tgc cta tgc gcc ttg ctc tct aac ttc tgt ccc tcc aca act gtg 160
Cys Cys Leu Cys Ala Leu Leu Ser Asn Phe Cys Pro Ser Thr Thr Val
-15 -10 -5 1
aaa gga gac gtc gtg act tcc ttc ttt cgt gct gac tat gac tta gcc 208
Lys Gly Asp Val Val Thr Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala
5 10 15
agt agg tct gca gat cag tcc tcc cag aaa gtg aag ttg cgc atg ttc 256
Ser Arg Ser Ala Asp Gln Ser Ser Gln Lys Val Lys Leu Arg Met Phe
20 25 30
act ggg cgt ctt ccc atc ggc ccc ttc gcc agt gtg ggg aac gcg gcg 304
Thr Gly Arg Leu Pro Ile Gly Pro Phe Ala Ser Val Gly Asn Ala Ala
35 40 45
gag ctg tgagccggcg actcgggtcc ctgaggtctg gattctttct ccgctactga 360
Glu Leu
50
gacacggcgg acacacacaa acacagaacc acacagccag tcccaggagc ccagtaatgg 420
agagcccaaa aaagaagaac cagcagctga aagtcgggat cctacacctg ggcagcagac 480
agaagaagat caggatacag ctgagatccc agtgcgcgac atggaagggtg atctgcaaga 540
gctgcatcag tcaaacaccg gggataaatc tggatttggg ttccggcgctc aagggtgaaga 600
taatacctaa agaggaacac tgtaaaatgc cagaagcagg tgaagagcaa ccacaagttt 660
aatgaagac aagctgaaac aacgcaagct ggttttatat tagatatttg acttaaacta 720
tctcaataaa gttttgcagc tttcaccaaaa aaaaaaaaaa aa 762

<210> 28
<211> 1102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..906

<220>
<221> sig_peptide
<222> 310..357
<223> Von Heijne matrix
score 11.0931109030915
seq FPLLLLSLGLVLA/EA

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gatcttttca gttgagagac ttcagctgtt cattgctcat ttggacttag ttcaagggtca 120
tgtcaaagaa gaagggtgcac ttacgctagt tgtagctct gtcttttgta accatcaagt 180
tccatgcgat tgatcagatt taggaggggg cggtggggga taatcaattt tgggtgtcac 240
caggtaaaca gagccctcag catctgaata gaaactgaac aggaacagaa gagattcact 300
acatctgag atg gag acc ttt cct ctg ctg ctc agc ctg ggc ctg gtt 351
Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val
-15 -10 -5
ctt gca gaa gca tca gaa agc aca atg aag ata att aaa gaa gaa ttt 399
Leu Ala Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe
1 5 10
aca gac gaa gag atg caa tat gac atg gca aaa agt ggc caa gaa aaa 447
Thr Asp Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys
15 20 25 30
cag acc att gag ata tta atg aac ccg atc ctg tta gtt aaa aat acc 495
Gln Thr Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr

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          35          40          45
agc ctc agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc      543
Ser Leu Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe
          50          55          60
aga agt tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac      591
Arg Ser Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp
          65          70          75
aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca      639
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala
          80          85          90
aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa      687
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu
          95          100          105          110
gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat      735
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn
          115          120          125
cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc      783
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys
          130          135          140
cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt      831
Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val
          145          150          155
acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg      879
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met
          160          165          170
agc tgg tta gtt tgt ggc tct aag ttg taaatccac agagctttag      926
Ser Trp Leu Val Cys Gly Ser Lys Leu
          175          180
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atatctactc tttagcacta tagtgaactc ctgattatct attctaactg gaggagtga      1046
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 seq ILMRDFSPSGIFG/AF

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          -35          -30
aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg      101
Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met
          -25          -20          -15
cgg gac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac      149
Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr
          -10          -5          1          5

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tac cgg tac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg      197
Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser
      10      15      20
ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt      245
Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
      25      30      35
tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac      287
Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
      40      45      50
tgaagaggac acactctgca cccccccacc ccacgacctt ggcccgagcc cctccgtgag      347
gaacacaatc tcaatcgttg ctgaatcctt tcatatccta ataggaatta acctccaaat      407
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gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg      170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
      -25      -20      -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc      218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
      -10      -5      1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag      266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
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ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac      314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
      25      30      35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag      362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
      40      45      50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg      410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
      55      60      65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc      458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
      70      75      80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta      506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85      90      95      100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac      554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn

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agc	tgc	agc	agt	gac	atc	gct	gac	gtg	gag	gtg	gac	atg	tcg	gga	gac	650
Ser	Cys	Ser	Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp	Met	Ser	Gly	Asp	
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Leu	Gly	Trp	Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile	Glu	Ser	Lys	Phe	
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Gln	Lys	Val	Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile	Gln	Lys	Ser	Val	
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Ser	Ser	Asp	Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Thr	Val	Thr	Thr	Glu	
			185						190					195		
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Ile	Asp	Ser	Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	Glu	Ala	Pro	Arg	
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Ala	Thr	Ala	Gln	Met	Leu	Glu	Val	Met	Phe	Lys	Gly	Glu	Ile	Phe	His	
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Arg	Asn	His	Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	Val	Met	Ser	Leu	
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cct	gag	gaa	cac	aac	aaa	atg	gtc	tac	ttt	gcc	atc	tcg	gat	tat	gtc	986
Pro	Glu	Glu	His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	Ser	Asp	Tyr	Val	
245					250					255					260	
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Phe	Asn	Thr	Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	Tyr	Leu	Asn	Phe	
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tcc	atc	aca	gat	gac	atg	ata	ccg	cct	gac	tct	aat	atc	cga	ctg	acc	1082
Ser	Ile	Thr	Asp	Asp	Met	Ile	Pro	Pro	Asp	Ser	Asn	Ile	Arg	Leu	Thr	
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Thr	Lys	Ser	Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro	
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Asn	Met	Asn	Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu	
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aac	ttc	agc	cct	ggg	aat	ctg	tct	gtg	gac	ccc	tat	atg	gag	ata	gat	1226
Asn	Phe	Ser	Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	Met	Glu	Ile	Asp	
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gcc	ttt	gtg	ctc	ctg	ccc	agc	tcc	agc	aag	gag	cct	gtc	ttc	cgg	ctc	1274
Ala	Phe	Val	Leu	Leu	Pro	Ser	Ser	Ser	Lys	Glu	Pro	Val	Phe	Arg	Leu	
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Ser	Val	Ala	Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	Asn	Thr	Ser	Lys	
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Ile	Thr	Gly	Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	Glu	Leu	Lys	Glu	
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tcc	aaa	ggt	gga	cta	ttc	aat	gca	gag	ctg	ttg	gaa	gcg	ctc	ctc	aac	1418
Ser	Lys	Val	Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	Ala	Leu	Leu	Asn	
		390				395					400					
tat	tac	atc	ctt	aac	acc	ttc	tac	ccc	aag	ttc	aat	gat	aag	ttg	gcc	1466
Tyr	Tyr	Ile	Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	Asp	Lys	Leu	Ala	
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Glu Gly Phe Pro Leu Pro Leu Leu Lys Arg Val Gln Leu Tyr Asp Leu	
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Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln	
440 445 450	
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Tyr Met Arg Val	
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Met	
gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca	167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser	
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Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser	
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caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa	311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu	
10 15 20	
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Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe	
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Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro	
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Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala	
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1114

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Met Ala Thr Gln Ala His Ser Leu Ser Tyr

-25

-20

gca ggg tgc aac ttc ttg tgc caa cgt ctg gtc ctg tct acc ctg agc 221
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Gly Arg Pro Val Lys Ile Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro
1 5 10 15

ggc ctc cga gat ttt gaa gcc agc ttc ata agg cta ttg gac aaa ata 317
Gly Leu Arg Asp Phe Glu Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile
20 25 30

acg aat ggt tct cga att gaa ata aac caa aca gga aca acc tta tat 365
Thr Asn Gly Ser Arg Ile Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr
35 40 45

tat cag cct ggc ctc ctg tat ggt gga tct gtg gaa cat gac tgt agc 413
Tyr Gln Pro Gly Leu Leu Tyr Gly Gly Ser Val Glu His Asp Cys Ser
50 55 60

gtc ctt cgt ggc att ggg tat tac ctg gag agt ctt ctt tgc ttg gct 461
Val Leu Arg Gly Ile Gly Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala
65 70 75

cca ttt atg aag cac ccg tta aaa ata gtt cta cga gga gtg acc aat 509
Pro Phe Met Lys His Pro Leu Lys Ile Val Leu Arg Gly Val Thr Asn
80 85 90 95

gat cag att gac cct tca gtt gat gtt ctt aag gca aca gca ctc cct 557
Asp Gln Ile Asp Pro Ser Val Asp Val Leu Lys Ala Thr Ala Leu Pro
100 105 110

ttg ttg aaa caa ttt ggg att gat ggt gaa tca ttt gaa ctg aag att 605
Leu Leu Lys Gln Phe Gly Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile
115 120 125

gtg cga cgg gga atg cct ccc gga gga gga ggc gaa gtg gtt ttc tca 653
Val Arg Arg Gly Met Pro Pro Gly Gly Gly Glu Val Val Phe Ser
130 135 140

tgt cct gtg agg aag gtc ttg aag ccc att caa ctc aca gat cca gga 701
Cys Pro Val Arg Lys Val Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly
145 150 155

aaa atc aaa cgt att aga gga atg gcg tac tct gta cgt gtg tca cct 749

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Gln	Met	Ala	Asn	Arg	Ile	Val	Asp	Ser	Ala	Arg	Ser	Ile	Leu	Asn	Lys	
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Phe	Ile	Pro	Asp	Ile	Tyr	Ile	Tyr	Thr	Asp	His	Ile	Lys	Gly	Val	Asn	
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Ser	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Leu	Ser	Leu	Val	Ala	Glu	Thr	Thr	
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Gly	Ala	Ala	Val	Leu	Pro	Glu	Asp	Leu	Gly	Arg	Asn	Cys	Ala	Arg	Leu	
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Leu	Leu	Glu	Glu	Ile	Tyr	Arg	Gly	Gly	Cys	Val	Asp	Ser	Thr	Asn	Gln	
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Ser	Leu	Ala	Leu	Leu	Leu	Met	Thr	Leu	Gly	Gln	Gln	Asp	Val	Ser	Lys	
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Val	Leu	Leu	Gly	Pro	Leu	Ser	Pro	Tyr	Thr	Ile	Glu	Phe	Leu	Arg	His	
		290					295					300				
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Leu	Lys	Ser	Phe	Phe	Gln	Ile	Met	Phe	Lys	Ile	Glu	Thr	Lys	Pro	Cys	
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ggt	gaa	gaa	ctc	aag	ggt	ggg	gat	aaa	gtg	ctg	atg	acc	tgt	ggt	ggc	1229
Gly	Glu	Glu	Leu	Lys	Gly	Gly	Asp	Lys	Val	Leu	Met	Thr	Cys	Val	Gly	
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                               -25                -20
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Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala
                               -15                -10                -5
aca gct ctt gct gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc      151
Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
      1                5                10
aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa      199
Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
      15                20                25                30
atg gaa ggt cac tat gtt cat gct ggg aac atc att gca aca cag cgc      247
Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
      35                40                45
cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc      295
His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
      50                55                60
ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccctaa gcatggtaat      346
Pro Leu Phe Pro Phe Leu Gly
      65
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aaa                                                                409

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ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaataca tggaaa atg      179
                               Met
                               -20
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt      227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
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Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
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gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
      15      20      25
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
      30      35      40      45
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
      50      55      60
tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
      65      70      75
tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515
Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
      80      85      90
atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
      95      100      105
tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
      110      115      120      125
gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
      130      135      140
act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
      145      150      155
cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
      160      165      170
ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg 807
Phe Ser Pro Ala
      175
atagtgata aatgaaaaaa aaaaaaaaaa 836

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 <213> Homo sapiens

<220>
 <221> CDS
 <222> 208..1239

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 <223> Von Heijne matrix
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 seq GLVLICVCSKTHS/LK

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tggaagaacc atgtccggca gctactgggc atgccaggca cacactgctg cccaagagga 120
gctgctgttt gaattatctg tgaatgttgg gaagaggaat gccagagctg ccggctgaaa 180

```

attacccaac caagagaaat ctgcagg atg gac ttt ctg gtc ctc ttc ttg ttc	234
Met Asp Phe Leu Val Leu Phe Leu Phe	
-25	
tac ctg gct tcg gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc tcg	282
Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys Ser	
-20 -15 -10 -5	
aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata ttt	330
Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile Phe	
1 5 10	
tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg ctt	378
Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu Leu	
15 20 25	
cat tac ctt ttc cat acg aga aac cac acc ttc att gtc ctg cac ctg	426
His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His Leu	
30 35 40	
gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt ggc	474
Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe Gly	
45 50 55 60	
tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc tat	522
Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro Tyr	
65 70 75	
ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga acc	570
Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly Thr	
80 85 90	
aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat gtt	618
Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His Val	
95 100 105	
tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct act	666
Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser Thr	
110 115 120	
tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt aac	714
Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys Asn	
125 130 135 140	
tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac tgc	762
Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn Cys	
145 150 155	
atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc ttg	810
Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu	
160 165 170	
acg gcc tcg gct gcc acc gtc gcc att gtg agc acc act ttt ctg gtc	858
Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu Val	
175 180 185	
cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat gac	906
His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp	
190 195 200	
ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac ctg	954
Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr Leu	
205 210 215 220	
ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg gtt	1002
Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val Val	
225 230 235	
ctg agc ttc ctc ctg ggt ggc tac ctg ttg ttt gtc ctg tat ctg gcg	1050
Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu Ala	
240 245 250	
gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc tgg	1098
Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala Trp	
255 260 265	
tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc caa	1146

Figure 1 consists of 12 subplots, labeled (a) through (l), each showing a histogram of the number of non-zero elements in the rows of the matrix A_k for $k = 0, 1, \dots, 11$. The x-axis for all plots is 'Number of non-zero elements' with major ticks at 0, 20, 40, 60, 80, and 100. The y-axis is 'Frequency' with major ticks at 0, 2, 4, 6, 8, and 10. The histograms show a distribution of non-zero elements per row, which is roughly bell-shaped and centered around 50-60 non-zero elements. The distributions for different k values are very similar, indicating a consistent sparsity pattern across the sequence of matrices.

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<221> CDS  
<222> 60..1682
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[illegible]

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Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	
		135					140					145				
tgg	gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	ggt	635
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	
	150					155				160						
ctg	gtg	ctc	tgc	tat	ggt	att	tat	ttc	aca	aag	tta	ctg	ggt	tcc	cca	683
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	
165					170					175					180	
gaa	tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	731
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	
			185						190				195			
tta	ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	779
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	
		200					205					210				
aaa	ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	827
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	
		215					220					225				
aca	gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	875
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	
	230					235				240						
ggt	gat	cag	ggt	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	923
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Leu	Gly	Ser	Leu	Val		
245				250					255				260			
gcc	aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	971
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	
			265				270						275			
gct	aag	gtg	ctg	gag	agg	gga	aag	gat	gcc	aca	ctt	cag	aag	cag	gag	1019
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	
		280					285					290				
gac	gtt	gct	gtg	gct	gct	gca	gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	1067
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	
		295					300					305				
ctg	ctg	gcc	ggc	ctg	acc	atc	act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	1115
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	
	310				315					320						
ctg	gct	ctg	gat	atc	tac	gga	ggg	acc	atg	ctt	agc	tca	gga	tcc	ggt	1163
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	
325				330					335				340			
cct	gtt	ttg	ctg	cgt	tcc	tac	tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	1211
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	
			345						350				355			
aat	gga	gtg	aca	gag	tgt	ttc	aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	1259
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	
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gtc	gac	agg	tac	aat	ttt	gtg	atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	1307
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	
		375				380						385				
gtg	tta	tcc	tat	ctc	ttg	acc	cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	1355
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	
	390				395					400						
ttg	gcc	aac	tgc	ttt	aac	atg	ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	1403
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	
405				410					415					420		
ttc	atc	cac	cgc	tac	tac	cga	agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	1451
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	
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Leu His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly
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ggt act gct gtt tgc gag gta ttc ctc tgc tgt gag cag ggc tgg cca      1547
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
      455      460      465
gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act      1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
      470      475      480
ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg      1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
      485      490      495      500
act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg      1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
      505      510
gaagcctgga caccgcaggc acctggacca gctatgggta gttctgtggg tggaacacat      1752
tctgtgtaag agcccccactg agggctctgc agcggagtga cagcaacccc agagatgagg      1812
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg      1872
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atcgatggta gctataagag tcgtgtctga acccggtctt tccaattggc ctgctccatc      180
cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg      230
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      -20      -15
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Leu Leu Leu Gly Pro Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser
      -10      -5      1
cag gat tgc gcg acg tgc agc tac cgc cta gtg cgc ccg gcc gac atc      326
Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
      5      10      15
aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg      374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
      20      25      30      35
aaa att tgg gaa acc tgc aag gag ctc ctg cag ctg tcc aaa cca gat      422
Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
      40      45      50
ctt cct caa gat ggc acc agc acc ctc aga gaa aat agc aaa ccg gaa      470
Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu

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cctggcataaa	ctgataggca	tgtatgggag	gaccacattc	ctggggacag	cctggggtatg	60										
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gggcttccct	ggaggtaaag	agctaggggtg	gggtggcagt	gggtagaacc	ccagctggac	180										
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gacaaatggg	gcttcttcag	cacagggtag	tgagtgctga	gctaagcaag	gacactgtcc	300										
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tacatccagt	ggctcaacgg	ctccctcata	catggcctct	ggaaccttgt	ttttctcttc	480										
tccaacctgt	ccctcatctt	cctc	atg	ccc	ttt	gca	tat	ttc	ttc	act	gag	531				
			Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	Glu					
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Glu	Thr	Val	Val	Met	Leu	Met	Leu	Leu	Thr	Leu	Leu	Val	Leu	Gly	Met	
	-15				-10					-5					1	
gtg	tgg	gtg	gca	tca	gcc	att	gtg	gac	aag	aac	aag	gcc	aac	aga	gag	675
Val	Trp	Val	Ala	Ser	Ala	Ile	Val	Asp	Lys	Asn	Lys	Ala	Asn	Arg	Glu	
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Ser	Leu	Tyr	Asp	Phe	Trp	Glu	Tyr	Tyr	Leu	Pro	Tyr	Leu	Tyr	Ser	Cys	
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Ile	Ser	Phe	Leu	Gly	Val	Leu	Leu	Leu	Leu	Val	Cys	Thr	Pro	Leu	Gly	
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Leu	Ala	Arg	Met	Phe	Ser	Val	Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	
	50				55					60					65	
ctg	ctg	gaa	gac	ctg	gag	gag	cag	ctg	tac	tgc	tca	gcc	ttt	gag	gag	867
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gca	gcc	ctg	acc	cgc	agg	atc	tgt	aat	cct	act	tcc	tgc	tgg	ctg	cct	915
Ala	Ala	Leu	Thr	Arg	Arg	Ile	Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	
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Leu	Asp	Met	Glu	Leu	Leu	His	Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	
		100					105					110				
agg	gtc	ctg	ctg	gag	aag	agg	cgg	aag	gct	tca	gcc	tgg	caa	cgg	aac	1011
Arg	Val	Leu	Leu	Glu	Lys	Arg	Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	
	115				120						125					
ctg	ggc	tac	ccc	ctg	gct	atg	ctg	tgc	ttg	ctg	ctg	ctg	acg	ggc	ctg	1059
Leu	Gly	Tyr	Pro	Leu	Ala	Met	Leu	Cys	Leu	Leu	Val	Leu	Thr			

210					215					220					225					
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Ile	Gly	Asn	Cys	Val	Cys	Leu	Leu	Val	Leu	Ser	Ser	Ala	Leu	Pro	Val					
				230					235					240						
ttc	tct	cga	acc	ctg	ggg	ctc	act	cgc	ttt	gac	ctg	ctg	ggt	gac	ttt				1395	
Phe	Ser	Arg	Thr	Leu	Gly	Leu	Thr	Arg	Phe	Asp	Leu	Leu	Gly	Asp	Phe					
				245					250					255						
gga	cgc	ttc	aac	tgg	ctg	ggc	aat	ttc	tac	att	gtg	ttc	ctc	tac	aac				1443	
Gly	Arg	Phe	Asn	Trp	Leu	Gly	Asn	Phe	Tyr	Ile	Val	Phe	Leu	Tyr	Asn					
				260					265					270						
gca	gcc	ttt	gca	ggc	ctc	acc	aca	ctc	tat	ctg	gtg	aag	acc	ttc	act				1491	
Ala	Ala	Phe	Ala	Gly	Leu	Thr	Thr	Leu	Tyr	Leu	Val	Lys	Thr	Phe	Thr					
				275					280					285						
gca	gct	gtg	cgg	gca	gag	ctg	atc	cgg	gcc	ttt	ggg	ctg	gac	aga	ctg				1539	
Ala	Ala	Val	Arg	Ala	Glu	Leu	Ile	Arg	Ala	Phe	Gly	Leu	Asp	Arg	Leu					
290					295					300					305					
ccg	ctg	ccc	gtc	tcc	ggt	ttc	ccc	cag	gca	tct	agg	aag	acc	cag	cac				1587	
Pro	Leu	Pro	Val	Ser	Gly	Phe	Pro	Gln	Ala	Ser	Arg	Lys	Thr	Gln	His					
				310					315					320						
cag	tgacctccag	ctgggggtgg	gaagaaaaaa	actggacact	gccatctgct											1640				
Gln																				
gccttaggcct	ggaggggaagc	ccaaggctac	ttggacctca	ggacctggaa	tctgagaggg														1700	
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cagagcctaa	gcactgtgct	atcctggagg	ggctttggac	cacctgaaag	accaagggga														2060	
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aaaa																2120				

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<212> DNA
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score 6.39000252120129
seq LGLSVLLTAATVA/GV
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aggccgcggc cgccagcgtg ggg atg tct agg agc tcg aag gtg gtg ctg ggc      113
                Met Ser Arg Ser Ser Lys Val Val Leu Gly
                -20                               -15

ctc tcg gtg ctg ctg acg gcg gcc aca gtg gcc ggc gta cat gtg aag      161
Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val Lys
-10                -5                1                5

cag cag tgg gac cag cag agg ctt cgt gac gga gtt atc aga gac att      209
Gln Gln Trp Asp Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile
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[illegible]

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<220>  
<221> CDS  
<222> 56..1678
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Met																
ggc agc cag gag gtg ctg ggc cac gcg gcc cgg ctg gcc tcc tcc ggt																106
Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly																
-25 -20 -15																
ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat gca																154
Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn Ala																
-10 -5 1 5																
ttt att ctt cgc ttc ctg tca aag gaa atc gtt ggc gta gta aat gta																202
Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val																
10 15 20																
aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc																250
Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala																
25 30 35																
ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc cag																298
Phe Arg Arg Ala Cys Leu Ser Gly Thr Gln Arg Asp Trp Ser Gln																
40 45 50																

acc	ctc	aac	ctg	ctg	tgg	cta	aca	gtc	ccc	ctg	ggg	gtg	ttt	tgg	tcc	346
Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp	Ser	
55						60					65					
tta	ttc	ctg	ggc	tgg	atc	tgg	ttg	cag	ctg	ctt	gaa	gtg	cct	gat	cct	394
Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp	Pro	
70					75					80					85	
aat	gtt	gtc	cct	cac	tat	gca	act	gga	gtg	gtg	ctg	ttt	ggg	ctc	tcg	442
Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu	Ser	
				90					95					100		
gca	gtg	gtg	gag	ctt	cta	gga	gag	ccc	ttt	tgg	gtc	ttg	gca	caa	gca	490
Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln	Ala	
			105					110					115			
cat	atg	ttt	gtg	aag	ctc	aag	gtg	att	gca	gag	agc	ctg	tcg	gta	att	538
His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val	Ile	
		120					125					130				
ctt	aag	agc	gtt	ctg	aca	gct	ttt	ctc	gtg	ctg	tgg	ttg	cct	cac	tgg	586
Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	Trp	
	135					140					145					
gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	gtt	ctg	634
Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	Leu	
				155						160					165	
gtg	ctc	tgc	tat	gtt	att	tat	ttc	aca	aag	tta	ctg	ggg	tcc	cca	gaa	682
Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	Glu	
				170					175					180		
tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	tta	730
Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	
			185					190					195			
ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	778
Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	
		200					205					210				
ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	826
Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	
	215					220					225					
gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	ggg	874
Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	
	230				235					240					245	
gat	cag	ggg	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	922
Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	Ala	
				250					255					260		
aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat					


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Gly Val Thr Glu Cys Phe Thr Phe Ala Ala Met Ser Lys Glu Glu Val
      360      365      370
gac agg tac aat ttt gtg atg ctg gcc ctg tcc tcc tca ttc ctg gtg      1306
Asp Arg Tyr Asn Phe Val Met Leu Ala Leu Ser Ser Ser Phe Leu Val
      375      380      385
tta tcc tat ctc ttg acc cgt tgg tgt ggc agc gtg ggc ttc atc ttg      1354
Leu Ser Tyr Leu Leu Thr Arg Trp Cys Gly Ser Val Gly Phe Ile Leu
      390      395      400      405
gcc aac tgc ttt aac atg ggc att cgg atc acg cag agc ctt tgc ttc      1402
Ala Asn Cys Phe Asn Met Gly Ile Arg Ile Thr Gln Ser Leu Cys Phe
      410      415      420
atc cac cgc tac tac cga agg agc ccc cac agg ccc ctg gct ggc ctg      1450
Ile His Arg Tyr Tyr Arg Arg Ser Pro His Arg Pro Leu Ala Gly Leu
      425      430      435
cac cta tcg cca gtc ctg ctc ggg aca ttt gcc ctc agt ggt ggg gtt      1498
His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly Val
      440      445      450
act gct gtt tcg gag gta ttc ctc tgc tgt gag cag ggc tgg cca gcc      1546
Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro Ala
      455      460      465
aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act ctc      1594
Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr Leu
      470      475      480      485
ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg act      1642
Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg Thr
      490      495      500
cag tta ggt gtg ccc aga cgc act gac aaa atg acg tgacttcagg      1688
Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
      505      510
gaagcctgga caccgagggc acctggacca gctatgggta gttctgtggg tggaacacat      1748
tctgtgtaag agccccactg agggctctgc agcggagtga cagcaacccc agagatgagg      1808
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg      1868
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tatagtgaata aaaaaaaaaa aaaaaa      1953

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<210> 42

<211> 1688

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 119..1522

<220>

<221> sig_peptide

<222> 119..181

<223> Von Heijne matrix

score 11.6921972463885

seq LLLCLALSGAAET/KP

<400> 42

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gcagcgtagg actgtggaga agggcggtgg gcaaggaggg aactcgagag cagcctcc      118
atg ggc aca cag gag ggc tgg tgc ctg ctc tgc ctg gct cta tct      166
Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
      -20      -15      -10
gga gca gca gaa acc aag ccc cac cca gca gag ggg cag tgg cgg gca      214

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Gly	Ala	Ala	Glu	Thr	Lys	Pro	His	Pro	Ala	Glu	Gly	Gln	Trp	Arg	Ala		
-5					1				5					10			
gtg	gac	gtg	gtc	cta	gac	tgt	ttc	ctg	gtg	aag	gac	ggg	gcg	cac	cgt		262
Val	Asp	Val	Val	Leu	Asp	Cys	Phe	Leu	Val	Lys	Asp	Gly	Ala	His	Arg		
			15					20					25				
gga	gct	ctc	gcc	agc	agt	gag	gac	agg	gca	agg	gcc	tcc	ctt	gtg	ctg		310
Gly	Ala	Leu	Ala	Ser	Ser	Glu	Asp	Arg	Ala	Arg	Ala	Ser	Leu	Val	Leu		
		30					35					40					
aag	cag	gtg	cca	gtg	ctg	gac	gat	ggc	tcc	ctg	gag	gac	ttc	acc	gat		358
Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp		
	45					50					55						
ttc	caa	ggg	ggc	aca	ctg	gcc	caa	gat	gac	cca	cct	att	atc	ttt	gag		406
Phe	Gln	Gly	Gly	Thr	Leu	Ala	Gln	Asp	Asp	Pro	Pro	Ile	Ile	Phe	Glu		
60					65				70						75		
gcc	tca	gtg	gac	ctg	gtc	cag	att	ccc	cag	gcc	gag	gcc	ttg	ctc	cat		454
Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu	Ala	Leu	Leu	His		
				80					85				90				
gct	gac	tgc	agt	ggg	aag	gag	gtg	acc	tgt	gag	atc	tcc	cgc	tac	ttt		502
Ala	Asp	Cys	Ser	Gly	Lys	Glu	Val	Thr	Cys	Glu	Ile	Ser	Arg	Tyr	Phe		
			95					100					105				
ctc	cag	atg	aca	gag	acc	act	gtt	aag	aca	gca	gct	tgg	ttc	atg	gcc		550
Leu	Gln	Met	Thr	Glu	Thr	Thr	Val	Lys	Thr	Ala	Ala	Trp	Phe	Met	Ala		
		110					115					120					
aac	gtg	cag	gtc	tct	gga	ggg	gga	cct	agc	atc	tcc	ttg	gtg	atg	aag		598
Asn	Val	Gln	Val	Ser	Gly	Gly	Gly	Pro	Ser	Ile	Ser	Leu	Val	Met	Lys		
		125				130					135						
act	ccc	agg	gtc	gcc	aag	aat	gag	gtg	ctc	tgg	cac	cca	acg	ctg	aac		646
Thr	Pro	Arg	Val	Ala	Lys	Asn	Glu	Val	Leu	Trp	His	Pro	Thr	Leu	Asn		
					145				150						155		
ttg	cca	ctg	agc	ccc	cag	ggg	act	gtg	cga	act	gca	gtg	gag	ttc	cag		694
Leu	Pro	Leu	Ser	Pro	Gln	Gly	Thr	Val	Arg	Thr	Ala	Val	Glu	Phe	Gln		
				160					165					170			
gtg	atg	aca	cag	acc	caa	tcc	ctg	agc	ttc	ctg	ctg	ggg	tcc	tca	gcc		742
Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala		
			175					180					185				
tcc	ttg	gac	tgt	ggc	ttc	tcc	atg	gca	ccg	ggc	ttg	gac	ctc	atc	agt		790
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser		
		190					195					200					
gtg	gag	tgg	cga	ctg	cag	cac	aag	ggc	agg	ggg	cag	ttg	gtg	tac	agc		838
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser		
		205				210					215						
tgg	acc	gca	ggg	cag	ggg	cag	gct	gtg	cgg	aag	ggc	gct	acc	ctg	gag		886
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu		
					225				230						235		
cct	gca	caa	ctg	ggc	atg	gcc	agg	gat	gcc	tcc	ctc	acc	ctg	ccc	ggc		934
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly		
				240					245					250			
ctc	act	ata	cag	gac	gag	ggg	acc	tac	att	tgc	cag	atc	acc	acc	tct		982
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser		
			255					260					265				
ctg	tac	cga	gct	cag	cag	atc	atc	cag	ctc	aac	atc	caa	gct	tcc	cct		1030
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro		
		270					275					280					
aaa	gta	cga	ctg	agc	ttg	gca	aac	gaa	gct	ctg	ctg	ccc	acc	ctc	atc		1078
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile		
		285				290					295						
tgc	gac	att	gct	ggc	tat	tac	cct	ctg	gat	gtg	gtg	gtg	acg	tgg	acc		1126
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr		

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300          305          310          315
cga gag gag ctg ggt gga tcc cca gcc caa gtc tct ggt gcc tcc ttc      1174
Arg Glu Glu Leu Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe

          320          325          330
tcc agc ctc agg caa agc gtg gca ggc acc tac agc atc tcc tcc tct      1222
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser

          335          340          345
ctc acc gca gaa cct ggc tct gca ggt gcc act tac acc tgc cag gtc      1270
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val

          350          355          360
aca cac atc tct ctg gag gag ccc ctt ggg gcc agc acc cag gtt gtc      1318
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val

          365          370          375
cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc      1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu

380          385          390          395
ttc ctt ctt gca ctg atg ttc ctg ggg ctt cag aga cgg caa gca cct      1414
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro

          400          405          410
aca gga ctt ggg ctg ctt cag gct gaa cgc tgg gag acc act tcc tgt      1462
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys

          415          420          425
gct gac aca cag agc tcc cat ctc cat gaa gac cgc aca gcg cgt gta      1510
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val

          430          435          440
agc cag ccc agc tgacctaaag cgacatgaga ctactagaaa gaaacgacac      1562
Ser Gln Pro Ser

          445
ccttcccaaa gccccacag ctactccaac ccaaacaaca accaagccag tttaatggta      1622
ggaatttgta ttttttgctt ttgttcagaa tacatgacat tggtaaataa aaaaaaaaaa      1682
aaaaaa      1688

<210> 43
<211> 1942
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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<220>
<221> sig_peptide
<222> 334..426
<223> Von Heijne matrix
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      seq TVFLLVTLQALDT/VE

<400> 43
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aatttttttg attccttctt atttgagaa atctccagct gctctgatca tagcctaaga      120
agactgcatg ctgcttcttc tcatgccaa gccagacct ctcacaacct cggatctcag      180
tccttcatgg agacctggtc ccagcaggaa tggcagtgcg ggaaattggc gccagatgg      240
ttcttccatg tgaagtgtc tcgggctctg ggctgacgag agaacacctg gtaaccaggt      300
tagccctctg tcagtcaccc agggcagggc agc atg gtg cgg att cag agg agg      354
                        Met Val Arg Ile Gln Arg Arg
                        -30                        -25

aag ctt ttg gca tct tgc ctg tgc gtc aca gcc acc gtc ttt ctg ctt      402

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Lys	Leu	Leu	Ala	Ser	Cys	Leu	Cys	Val	Thr	Ala	Thr	Val	Phe	Leu	Leu	
				-20					-15					-10		
gtc	aca	ctc	cag	gcc	ttg	gat	acc	gtt	gag	aat	cta	atg	aaa	gtc	acg	450
Val	Thr	Leu	Gln	Ala	Leu	Asp	Thr	Val	Glu	Asn	Leu	Met	Lys	Val	Thr	
			-5					1			5					
ggc	cct	ccc	cag	gga	gtt	aca	gac	tcc	atg	caa	tgc	ttc	aat	gat	cag	498
Gly	Pro	Pro	Gln	Gly	Val	Thr	Asp	Ser	Met	Gln	Cys	Phe	Asn	Asp	Gln	
	10				15					20						
tgg	cct	tta	tct	aac	acc	agg	agc	agc	gag	cac	ata	aaa	gag	gtc	atg	546
Trp	Pro	Leu	Ser	Asn	Thr	Arg	Ser	Ser	Glu	His	Ile	Lys	Glu	Val	Met	
	25				30					35					40	
gtt	gag	ctg	ggg	aag	ttt	gaa	agg	aag	gag	ttt	aaa	agt	tcc	agt	ttg	594
Val	Glu	Leu	Gly	Lys	Phe	Glu	Arg	Lys	Glu	Phe	Lys	Ser	Ser	Ser	Leu	
				45					50					55		
caa	gat	gga	cat	aca	aaa	atg	gag	gaa	gca	cct	acg	cat	ctt	aat	tca	642
Gln	Asp	Gly	His	Thr	Lys	Met	Glu	Glu	Ala	Pro	Thr	His	Leu	Asn	Ser	
			60					65					70			
ttt	ctt	aag	aaa	gaa	gga	ttg	acc	ttc	aac	agg	aaa	aga	aaa	tgg	gaa	690
Phe	Leu	Lys	Lys	Glu	Gly	Leu	Thr	Phe	Asn	Arg	Lys	Arg	Lys	Trp	Glu	
		75					80					85				
ttg	gac	agc	tac	ccc	att	atg	ctc	tgg	tgg	tcc	ccg	ctg	acg	ggg	gag	738
Leu	Asp	Ser	Tyr	Pro	Ile	Met	Leu	Trp	Trp	Ser	Pro	Leu	Thr	Gly	Glu	
	90					95				100						
act	ggg	agg	tta	ggc	caa	tgt	gga	gca	gat	gct	tgt	ttc	ttc	acc	atc	786
Thr	Gly	Arg	Leu	Gly	Gln	Cys	Gly	Ala	Asp	Ala	Cys	Phe	Phe	Thr	Ile	
	105				110					115					120	
aac	cgg	acc	tac	ctc	cat	cat	cac	atg	acc	aaa	gca	ttc	ctc	ttc	tat	834
Asn	Arg	Thr	Tyr	Leu	His	His	His	Met	Thr	Lys	Ala	Phe	Leu	Phe	Tyr	
				125					130					135		
ggt	act	gac	ttt	aac	ata	gat	agc	tta	cct	ctg	cct	cgg	aaa	gcc	cat	882
Gly	Thr	Asp	Phe	Asn	Ile	Asp	Ser	Leu	Pro	Leu	Pro	Arg	Lys	Ala	His	
			140					145					150			
cat	gac	tgg	gct	gtt	ttt	cat	gaa	gag	tcc	ccg	aaa	aac	aat	tat	aag	930
His	Asp	Trp	Ala	Val	Phe	His	Glu	Glu	Ser	Pro	Lys	Asn	Asn	Tyr	Lys	
		155					160					165				
ctc	ttt	cat	aaa	cca	gtg	atc	acc	ttg	ttc	aac	tac	act	gcc	acg	ttc	978
Leu	Phe	His	Lys	Pro	Val	Ile	Thr	Leu	Phe	Asn	Tyr	Thr	Ala	Thr	Phe	
	170					175				180						
agc	agg	cat	tcc	cac	ttg	cca	cta	act	acc	caa	tac	ttg	gag	agc	att	1026
Ser	Arg	His	Ser	His	Leu	Pro	Leu	Thr	Thr	Gln	Tyr	Leu	Glu	Ser	Ile	
	185				190					195					200	
gaa	gtc	ctg	aag	tca	ctc	cga	tac	cta	gtt	cct	ttg	cag	tcc	aaa	aac	1074
Glu	Val	Leu	Lys	Ser	Leu	Arg	Tyr	Leu	Val	Pro	Leu	Gln	Ser	Lys	Asn	
				205					210					215		
aag	ctt	aga	aaa	aga	ctt	gct	ccg	ctg	gtg	tat	gta	cag	tca	tac	tgt	1122
Lys	Leu	Arg	Lys	Arg	Leu	Ala	Pro	Leu	Val	Tyr	Val	Gln	Ser	Tyr	Cys	
			220					225					230			
gac	cca	cca	tca	gac	agg	gac	agc	tat	gtt	cgc	gag	ctg	atg	act	tac	1170
Asp	Pro	Pro	Ser	Asp	Arg	Asp	Ser	Tyr	Val	Arg	Glu	Leu	Met	Thr	Tyr	
		235					240					245				
atc	gag	gtc	gat	tcc	tat	ggt	gaa	tgt	tta	cga	aac	aaa	gac	ctc	cct	1218
Ile	Glu	Val	Asp	Ser	Tyr	Gly	Glu	Cys	Leu	Arg	Asn	Lys	Asp	Leu	Pro	
	250					255				260						
cag	cag	ctg	aaa	aat	cca	gcc	tct	atg	gat	gcc	gat	ggc	ttt	tat	agg	1266
Gln	Gln	Leu	Lys	Asn	Pro	Gla	Ser	Met	Asp	Ala	Asp	Gly	Phe	Tyr	Arg	
	265				270					275					280	
atc	att	gca	cag	tat	aag	ttt	atc	cta	gct	ttt	gag	aat	gca	gtt	tgt	1314
Ile	Ile	Ala	Gln	Tyr	Lys	Phe	Ile	Leu	Ala	Phe	Glu	Asn	Ala	Val	Cys	

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                285                290                295
gat gac tac atc act gag aag ttc tgg agg cca ctg aaa ctg ggg gta      1362
Asp Asp Tyr Ile Thr Glu Lys Phe Trp Arg Pro Leu Lys Leu Gly Val
                300                305                310
gtc cct gta tat tac gga tcc ccc agc atc aca gac tgg ctt cca agt      1410
Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
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aac aaa agt gct att ctt gta tca gaa ttt tct cac ccc agg gaa ctg      1458
Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
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gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc      1506
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
345                350                355                360
tat gta gaa tgg aag ctg aag ggt aga tct cta acc agc gac ttc      1551
Tyr Val Glu Trp Lys Leu Lys Gly Arg Ser Leu Thr Ser Asp Phe
                365                370                375
tgacagctct caggggaacgg aaatggggag tgcaagacgt caaccaggac aattacatcg      1611
atgcatttga gtgtatggtg tgcaccaagg tgtgggctaa tatcaggctt caggaaaagg      1671
gcttaccacc caaaagatgg gaggcagaag ataccacact gagttgcca gagcccacag      1731
tgtttgcttt ctcaccactc cggactccac ctttgagctc tttgcgagag atgtggattt      1791
ccagctttga acaatccaag aaagaagccc aggcactaag gtggctggtt gataggaatc      1851
aaaacttttc atctcaagag ttttggggcc tagtattcaa ggactgattt caaaaatgat      1911
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 <213> Homo sapiens

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 seq GVGLVTLLGLAVG/SY

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                Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu
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ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc tac ttg      158
Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu
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gtt cgg agg tcc cgc cgg cct cag gtc act ctc ctg gac ccc aat gaa      206
Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu
                5                10                15
aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac aac acc      254
Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr
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aag agg ttc cgc ttt gcc ctg ccc acc gcc cac cac act ctg ggg ctg      302
Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu
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cct gtg ggc aaa cat atc tac ctc tcc acc cga att gat ggc agc ctg      350

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Pro	Val	Gly	Lys	His	Ile	Tyr	Leu	Ser	Thr	Arg	Ile	Asp	Gly	Ser	Leu		
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Val	Ile	Arg	Pro	Tyr	Thr	Pro	Val	Thr	Ser	Asp	Glu	Asp	Gln	Gly	Tyr		
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Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe		
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cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	gtt	ggg	494	
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly		
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Asp	Val	Val	Glu	Phe	Arg	Gly	Pro	Ser	Gly	Leu	Leu	Thr	Tyr	Thr	Gly		
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aaa	ggg	cat	ttt	aac	att	cag	ccc	aac	aag	aaa	tct	cca	cca	gaa	ccc	590	
Lys	Gly	His	Phe	Asn	Ile	Gln	Pro	Asn	Lys	Lys	Ser	Pro	Pro	Glu	Pro		
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cca	atg	cta	cag	ctg	atc	cgg	gcc	atc	ctg	aaa	gtc	cct	gaa	gat	cca	686	
Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	Asp	Pro		
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Thr	Gln	Cys	Phe	Leu	Phe	Ala	Asn	Gln	Thr	Glu	Lys	Asp	Ile	Ile			
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Leu	Arg	Glu	Asp	Leu	Glu	Glu	Leu	Gln	Ala	Arg	Tyr	Pro	Asn	Arg	Phe		
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aag	ctc	tgg	ttc	act	ctg	gat	cat	ccc	cca	aaa	gat	tgg	gcc	tac	agc	830	
Lys	Leu	Trp	Phe	Thr	Leu	Asp	His	Pro	Pro	Lys	Asp	Trp	Ala	Tyr	Ser		
			215					220					225				
aag	ggc	ttt	gtg	act	gcc	gac	atg	atc	cgg	gaa	cac	ctg	ccc	gct	cca	878	
Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	Ala	Pro		
		230				235						240					
ggg	gat	gat	gtg	ctg	gta	ctg	ctt	tgt	ggg	cca	ccc	cca	atg	gtg	cag	926	
Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	Val	Gln		
	245					250				255							
ctg	gcc	tgc	cat	ccc	aac	ttg	gac	aaa	ctg	ggc	tac	tca	caa	aag	atg	974	
Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	Lys	Met		
260				265				270						275			
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Arg	Phe	Thr	Tyr														
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aacagggtcca	ggagaggccc	atggagcagt	ctcttccatg	gagtaagaag	gaagggagca											1266	
tgtacgcttg	gtccaagatt	ggctagttcc	ttgatagcat	cttactctca	ccttctttgt											1326	
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atggagatgg	caagaaagga	ggaaatgatt	tcttcagatc	tcaaaggagt	ctgaaatatc											1506	
atatttctgt	gtgtgtctct	ctcagccctt	gcccaggcta	gagggaaaca	gctactgata											1566	
atcgaaaact	gctgtttgtg	gcaggaaccc	ctggctgtgc	aaataaatgg	ggctgaggcc											1626	
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<222> 157..1482

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<223> Von Heijne matrix

score 11.6921972463885

seq LLLCLALSGAAET/KP

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ggcgggtgggc aaggagggaa ctcgagagca gcctcc atg ggc aca cag gag ggc      174
                               Met Gly Thr Gln Glu Gly
                               -20
tgg tgc ctg ctg ctc tgc ctg gct cta tct gga gca gca gaa acc aag      222
Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys
-15                               -10                               -5                               1
ccc cac cca gca gag ggg cag ttg cgg gca gtg gac gtg gtc cta gac      270
Pro His Pro Ala Glu Gly Gln Leu Arg Ala Val Asp Val Val Leu Asp
                    5                               10                               15
tgc ttc ctg gcg aag gac ggt gcg cac cgt gga gct ctc gcc agc agt      318
Cys Phe Leu Ala Lys Asp Gly Ala His Arg Gly Ala Leu Ala Ser Ser
                20                               25                               30
gag gac agg gca agg gcc tcc ctt gtg ctg aag cag gtg cca gtg ctg      366
Glu Asp Arg Ala Arg Ala Ser Leu Val Leu Lys Gln Val Pro Val Leu
                35                               40                               45
gac gat ggc tcc ctg gag gac ttc acc gat ttc caa ggg ggc aca ctg      414
Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp Phe Gln Gly Gly Thr Leu
50                               55                               60                               65
gcc caa gat gac cca cct att atc ttt gag gcc tca gtg gac ctg gtc      462
Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu Ala Ser Val Asp Leu Val
                70                               75                               80
cag att ccc cag gcc gag gcc ttg ctc cat gct gac tgc agt ggg aag      510
Gln Ile Pro Gln Ala Glu Ala Leu Leu His Ala Asp Cys Ser Gly Lys
                85                               90                               95
gag gtg acc tgt gag atc tcc cgc tac ttt ctc cag atg aca gag acc      558
Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe Leu Gln Met Thr Glu Thr
                100                               105                               110
act gtt aag aca gca gct tgg ttc atg gcc aac atg cag gtc tct gga      606
Thr Val Lys Thr Ala Ala Trp Phe Met Ala Asn Met Gln Val Ser Gly
                115                               120                               125
ggg gga cst agc atc tcc ttg gtg atg aag act ccc agg gtc acc aag      654
Gly Gly Xaa Ser Ile Ser Leu Val Met Lys Thr Pro Arg Val Thr Lys
130                               135                               140                               145
aat gag gcg ctc tgg cac ccg acg ctg aac ttg cca ctg agc ccc cag      702
Asn Glu Ala Leu Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln
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ggg act gtg cga act gca gtg gag ttc cag gtg atg aca cag acc caa      750
Gly Thr Val Arg Thr Ala Val Glu Phe Gln Val Met Thr Thr Thr Gln
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tcc ctg agc ttc ctg ctg ggg tcc tca gcc tcc ttg gac tgt ggc ttc      798
Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe
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195 200 205	
cac aag ggc agg ggt cag ttg gtg tac agc tgg acc gca ggg cag ggg	894
His Lys Gly Arg Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly	
210 215 220 225	
cag gct gtg cgg aag ggc gct acc ctg gag cct gca caa ctg ggc atg	942
Gln Ala Val Arg Lys Gly Ala Thr Leu Glu Pro Ala Gln Leu Gly Met	
230 235 240	
gcc agg gat gcc tcc ctc acc ctg ccc ggc ctc act ata cag gac gag	990
Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu	
245 250 255	
ggg acc tac att tgc cag atc acc acc tct ctg tac cga gct cag cag	1038
Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln	
260 265 270	
atc atc cag ctc aac atc caa gct tcc cct aaa gta cga ctg agc ttg	1086
Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu	
275 280 285	
gca aac gaa gct ctg ctg ccc acc ctc atc tgc gac att gct ggc tat	1134
Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr	
290 295 300 305	
tac cct ctg gat gtg gtg gtg acg tgg acc cga gag gag ctg ggt gga	1182
Tyr Pro Leu Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly	
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Ser Pro Ala Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser	
325 330 335	
gtg gca ggc acc tac agc atc tcc tcc tct ctc acc gca gaa cct ggc	1278
Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly	
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tct gca ggt gcc act tac acc tgc cag gtc aca cac atc tct ctg gag	1326
Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val Thr His Ile Ser Leu Glu	
355 360 365	
gag ccc ctt ggg gcc agc acc cag gtt gtc cca cca gag cgg aga aca	1374
Glu Pro Leu Gly Ala Ser Thr Gln Val Val Pro Pro Glu Arg Arg Thr	
370 375 380 385	
gcc ttg gga gtc atc ttt gcc agc agt ctc ttc ctt ctt gca ctg atg	1422
Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met	
390 395 400	
ttc ctg ggg ctt cag aga cgg caa gca cct aca gga ctt ggg ctg ctt	1470
Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu	
405 410 415	
cag gct gaa cgc taggagacca cttcctgtgc tgacacacag agctcccatc	1522
Gln Ala Glu Arg	
420	
tccatgaaga ccgcacagcg cgtgtaagcc agcccagctg acctaaagcg acatgagact	1582
actagaaaga aacgacaccc ttccccaagc cccacagct actccaaccc aaacaacaac	1642
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<221> CDS

<222> 195..1052


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<222> 195..338
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ttccttagac aagacacagt gtagggcccg gcccggtgtg gccccaggac tcctttggaa      180
tatagctgtg gaca atg aat cct gcg agc gat ggg ggc aca tca gag agc      230
              Met Asn Pro Ala Ser Asp Gly Gly Thr Ser Glu Ser
              -45              -40
att ttt gac ctg gac tat gca tcc tgg ggg atc cgc tcc acg ctg atg      278
Ile Phe Asp Leu Asp Tyr Ala Ser Trp Gly Ile Arg Ser Thr Leu Met
      -35              -30              -25
gtc gct ggc ttt gtc ttc tac ttg ggc gtc ttt gtg gtc tgc cac cag      326
Val Ala Gly Phe Val Phe Tyr Leu Gly Val Phe Val Val Cys His Gln
      -20              -15              -10              -5
ctg tcc tct tcc ctg aat gcc act tac cgt tct ttg gtg gcc aga gag      374
Leu Ser Ser Ser Leu Asn Ala Thr Tyr Arg Ser Leu Val Ala Arg Glu
              1              5              10
aag gtc ttc tgg gac ctg gcg gcc acg cgt gca gtc ttt ggt gtt cag      422
Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln
              15              20              25
agc aca gcc gca ggc ctg tgg gct ctg ctg ggg gac cct gtg ctg cat      470
Ser Thr Ala Ala Gly Leu Trp Ala Leu Leu Gly Asp Pro Val Leu His
              30              35              40
gcc gac aag gcg cgt ggc cag cag aac tgg tgc tgg ttt cac atc acg      518
Ala Asp Lys Ala Arg Gly Gln Gln Asn Trp Cys Trp Phe His Ile Thr
      45              50              55              60
aca gca acg gga ttc ttt tgc ttt gaa aat gtt gca gtc cac ctg tcc      566
Thr Ala Thr Gly Phe Phe Cys Phe Glu Asn Val Ala Val His Leu Ser
              65              70              75
aac ttg atc ttc cgg aca ttt gac ttg ttt ctg gtt atc cac cat ctc      614
Asn Leu Ile Phe Arg Thr Phe Asp Leu Phe Leu Val Ile His His Leu
              80              85              90
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Phe Ala Phe Leu Gly Phe Leu Gly Cys Leu Val Asn Leu Gln Ala Gly
              95              100              105
cac tat cta gct atg acc acg ttg ctc ctg gag atg agc acg ccc ttt      710
His Tyr Leu Ala Met Thr Thr Leu Leu Leu Glu Met Ser Thr Pro Phe
              110              115              120
acc tgc gtt tcc tgg atg ctc tta aag gcg ggc tgg tcc gag tct ctg      758
Thr Cys Val Ser Trp Met Leu Leu Lys Ala Gly Trp Ser Glu Ser Leu
              125              130              135              140
ttt tgg aag ctc aac cag tgg ctg atg att cac atg ttt cac tgc cgc      806
Phe Trp Lys Leu Asn Gln Trp Leu Met Ile His Met Phe His Cys Arg
              145              150              155
atg gtt cta acc tac cac atg tgg tgg gtg tgt ttc tgg cac tgg gac      854
Met Val Leu Thr Tyr His Met Trp Trp Val Cys Phe Trp His Trp Asp
              160              165              170
ggc ctg gtc agc agc ctg tat ctg cct cat ttg aca ctg ttc ctt gtc      902
Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val
              175              180              185
gga ctg gct ctg ctt acg cta atc att aat cca tat tgg acc cat aag      950

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Gly Leu Ala Leu Leu Thr Leu Ile Ile Asn Pro Tyr Trp Thr His Lys
190 195 200
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Lys Thr Gln Gln Leu Leu Asn Pro Val Asp Trp Asn Phe Ala Gln Pro
205 210 215 220
gaa gcc aag agc agg cca gaa ggc aac ggg cag ctg ctg cgg aag aag 1046
Glu Ala Lys Ser Arg Pro Glu Gly Asn Gly Gln Leu Leu Arg Lys Lys
225 230 235
agg cca tagctgctcc agccgggggct ccgggggcggc agcagagctg gcacaccgat 1102
Arg Pro
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seq ALLWAQEVGQVLA/GR

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cagctgctgc atcccatggc caggggtggc gtccaggtgg cagagcagct aggaacgcaa 180
ggcctgaacc tggggccaga caccctctc ccggcc atg gtc aac gac cct cca 234
Met Val Asn Asp Pro Pro
-20
gta cct gcc tta ctg tgg gcc cag gag gtg ggc caa gtc ttg gca ggc 282
Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly
-15 -10 -5 1
cgt gcc cgc agg ctg ctg ctg cag ttt ggg gtg ctc ttc tgc acc atc 330
Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly Val Leu Phe Cys Thr Ile
5 10 15
ctc ctt ttg ctc tgg gtg tct gtc ttc ctc tat ggc tcc ttc tac tat 378
Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr
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tcc tat atg ccg aca gtc agc cac ctc agc cct gtg cat ttc tac tac 426
Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr

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Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val	
50					55					60					65	
gcc	aat	gtc	tcg	ctg	act	aag	ggg	gga	cgt	gat	cgg	gtg	ctg	atg	tat	522
Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	
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gga	cag	ccg	tat	cgt	gtt	acc	tta	gag	ctt	gag	ctg	cca	gag	tcc	cct	570
Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	
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gtg	aat	caa	gat	ttg	ggc	atg	ttc	ttg	gtc	acc	att	tcc	tgc	tac	acc	618
Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	
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aga	ggg	ggc	cga	atc	atc	tcc	act	tct	tcg	cgt	tcg	gtg	atg	ctg	cat	666
Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser	Arg	Ser	Val	Met	Leu	His	
	115					120					125					
tac	cgc	tca	gac	ctg	ctc	cag	atg	ctg	gac	aca	ctg	gtc	ttc	tct	agc	714
Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	
130					135					140					145	
ctc	ctg	cta	ttt	ggc	ttt	gca	gag	cag	aag	cag	ctg	ctg	gag	gtg	gaa	762
Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	
				150					155					160		
ctc	tac	gca	gac	tat	aga	gag	aac	tcg	tac	gtg	ccg	acc	act	gga	gcg	810
Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr	Val	Pro	Thr	Thr	Gly	Ala	
			165					170					175			
atc	att	gag	atc	cac	agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	858
Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	
			180				185					190				
cgc	atc	cac	gcg	cac	ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	906
Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	
	195					200					205					
ccg	atg	acc	tgc	gcc	ttc	ata	ggg	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	954
Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	
210					215					220					225	
agc	gtc	atc	gtg	ctc	ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	1002
Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	
				230					235					240		
tgg	ccc	cga	cac	cgc	ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	1050
Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	
			245					250					255			
aat	tcc	cgg	aag	gaa	gtc											

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gtc cta gag act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga      1386
Val Leu Glu Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg
      355                      360                      365
cag cgc ccc acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc      1440
Gln Arg Pro Thr Cys Ser Ser Ser
370                      375
agcactttcc cacctgactc ctctcccctc gtttttcctt caataaacta ttttgtgtca      1500
gcttcgaaaa aaaaaaaaaa aaa      1523

<210> 48
<211> 832
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..492

<220>
<221> sig_peptide
<222> 103..162
<223> Von Heijne matrix
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      seq LFFCYLLLFTCSG/VE

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gtttactcgc tgctgtgccc atctatcagc aggctccggg ctgaagattg cttctcttct      60
ctctctcaag gtctagtac ggagcccgcg cgcggcgcca cc atg cgg cag aag      114
                               Met Arg Gln Lys
                               -20
gcg gta tcg ctt ttc ttc tgc tac ctg ctg ctc ttc act tgc agt ggg      162
Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly
      -15                      -10                      -5
gtg gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc      210
Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser
1      5      10      15
ggg ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca      258
Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala
      20      25      30
gtc gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc      306
Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala
      35      40      45
aac tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg      354
Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly
      50      55      60
ggc ggc gtg ccc gcc ggg ggg cta gtg gcc acg ctg cag agc ctc ggg      402
Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly
      65      70      75      80
gct ggt ggc agc agc gtc gtc ata ggt aat att ggt gcc ctg atg ggc      450
Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly
      85      90      95
tac gcc acc cac aag tat ctc gat agt gag gag gat gag gag      492
Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
      100      105      110
tagccagcag ctcccagaac ctcttcttcc ttcttggect aactcttcca gttaggatct      552
agaactttgc cttttttttt tttttttttt tttttttgag atggggttctc actatattgt      612
ccaggctaga gtgcagtggc tattcacaga tgcgaacata gtacactgca gcttccaact      672
cctagcctca agtgatcttc ctgtctcaac ctcccaagta ggattacaag catgcgccga      732

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cgatgcccag aatccagaac tttgtctatc actctcccca acaacctaga tgtgaaaaca 792
gaataaaactt caccagaaa gcaaaaaaaaa aaaaaaaaaa 832

<210> 49
<211> 831
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 234..491

<220>
<221> sig_peptide
<222> 234..293
<223> Von Heijne matrix
score 4.85037394589162
seq AVAGLPALGFTGA/GI

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gtttactcgc tgctgtgccc atctatcagc aggctccggg ctgaagattg cttctcttct 60
ctcctccaag gtctagtac ggagcccgcg cgcggcgcca ccatgcggca gaaggcggtta 120
tcgcttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180
agtgtctcga gagctcggac agcggctccg ggttctggaa ggcctgacc ttc atg 236

Met

-20

gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284
Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe
-15 -10 -5

acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332
Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser
1 5 10

tgg tct gcg atc ctg aat ggg ggc ggc gtg ccc gcc ggg ggg cta gtg 380
Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val
15 20 25

gcc acg ctg cag agc ctc ggg gct ggt ggc agc agc gtc gtc ata ggt 428
Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly
30 35 40 45

aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476
Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser
50 55 60

gag gag gat gag gag tagccagcag ctcccagaac ctcttcttcc ttcttggcct 531
Glu Glu Asp Glu Glu
65

aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591

atgggttctc actatatgt ccaggctaga gtgcagtggc tattcacaga tgccaacata 651

gtacactgca gctccaact cctagcctca agtgatcctc ctgtctcaac ctccaagta 711

ggattacaag catgcgccga cgatgcccag aatccagaac tttgtctatc actctcccca 771

acaacctaga tgtgaaaaca gaataaaactt caccagaaa gcaaaaaaaaa aaaaaaaaaa 831

<210> 50
<211> 917
<212> DNA
<213> Homo sapiens

<220>
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<222> 180..800

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<220>
<221> sig_peptide
<222> 180..248
<223> Von Heijne matrix
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      seq ILLLLWLIAPSRA/CT

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ctgtgggttc cgcacccgct gccacccccg cccctagcgt ggacatttat cctctagcgc      120
tcaggccctg cgcgccatgc cgcagatcca gcgcccagag agacaccaga gaacccacc      179
atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg      227
Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
      -20                               -15                               -10
ctg ata gcc ccc agc agg gcc tgc acc tgt gtc cca ccc cac cca cag      275
Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
      -5                               1                               5
acg gcc ttc tgc aat tcc gac ctc gtc atc agg gcc aag ttc gtg ggg      323
Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
10                               15                               20                               25
aca cca gaa gtc aac cag acc acc tta tac cag cgt tat gag atc aag      371
Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
      30                               35                               40
atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac      419
Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
      45                               50                               55
atc cgg ttc gtc tac acc ccc gcc atg gag agt gtc tgc gga tac ttc      467
Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
      60                               65                               70
cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg      515
His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
      75                               80                               85
cag gat gga ctc ttg cac atc act acc tgc agt ttt gtg gct ccc tgg      563
Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
90                               95                               100                               105
aac agc ctg agc tta gct cag cgc cgg ggc ttc acc aag acc tac act      611
Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
      110                               115                               120
gtt ggc tgt gag gaa tgc aca gtg ttt ccc tgt tta tcc ttc ccc tgc      659
Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
      125                               130                               135
aaa ctg cag agt ggc act cat tgc ttg tgg acg gac cag ctc ctc caa      707
Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
      140                               145                               150
ggc tct gaa aag ggc ttc cag tcc cgt cac ctt gcc tgc ctg cct cgg      755
Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
      155                               160                               165
gag cca ggg ctg tgc acc tgg cag tcc ctg cgg tcc cag ata gcc      800
Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
170                               175                               180
tgaatcctgc cgggagtgga agctgaagcc tgcacagtgt ccaccctgtt cccactccca      860
tctttcttcc ggacaatgaa ataaagagtt accaccacgc aaaaaaaaaa aaaaaaa      917

<210> 51
<211> 621
<212> DNA
<213> Homo sapiens

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<220>
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 <222> 140..472

<220>
 <221> sig_peptide
 <222> 140..211
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 score 8.44884907465122
 seq FVVFSLFLICAMA/GD

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 attttttttt catatctgac atttctatgt cctatgacgg tttcacagct atcctacttt 60
 ggagaagatg ctggaaattc agagtttccg ccagagaata tatgcctgaa ctaaaagagg 120
 aagtgggtcta taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca 172
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser
 -20 -15
 ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta 220
 Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val
 -10 -5 1
 gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg 268
 Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala
 5 10 15
 ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa 316
 Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys
 20 25 30 35
 tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg 364
 Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp
 40 45 50
 att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc 412
 Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala
 55 60 65
 ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg 460
 Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val
 70 75 80
 aga ttt aac att tagaggtgac agcatecccc acactggcag ttaatttttt 512
 Arg Phe Asn Ile
 85
 gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat 572
 acaaataatta gttgaatgaa ttgttgaatt acaaaaaaaaa aaaaaaaaaa 621

<210> 52
 <211> 673
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..484

<220>
 <221> sig_peptide
 <222> 68..112
 <223> Von Heijne matrix
 score 4.93618539864455
 seq AVVFVFSLLDCCA/LI

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gaggagg atg gag gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc 109
      Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys
      -15                -10                -5
gcg ctc atc ttc ctc tcg gtc tac ttc ata att aca ttg tct gat tta 157
Ala Leu Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu
      1                5                10                15
gaa tgt gat tac att aat gct aga tca tgt tgc tca aaa tta aac aag 205
Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys
      20                25                30
tgg gta att cca gaa ttg att ggc cat acc att gtc act gta tta ctg 253
Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu
      35                40                45
ctc atg tca ttg cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc 301
Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala
      50                55                60
act tgg aat ata tat cga tac att atg gtg ccg agt ggt aac atg gga 349
Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly
      65                70                75
gtg ttt gat cca aca gaa ata cac aat cga ggg cag ctg aag tca cac 397
Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His
      80                85                90                95
atg aaa gaa gcc atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc 445
Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe
      100                105                110
atg tat ctt tat agt atg atc tta gct ttg ata aat gac tgaagctgga 494
Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
      115                120
gaagccgtgg ttgaagtcag cctacactac agtgcacagt tgaggagcca gagacttctt 554
aaatcatcct tagaaccgtg accatagcag tatatatattt cctcttgga caaaaaacta 614
tttttgctgt atttttacca tataaagtat ttaaaaaaca cgaaaaaaa aaaaaaaa 673

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<210> 53
<211> 897
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 38..517

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<220>
<221> sig_peptide
<222> 38..118
<223> Von Heijne matrix
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      seq VLWLSGLSEPGAA/RQ

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      Met Gln Arg Val Ser Gly
      -25
ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc tct 103
Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser
      -20                -15                -10
gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg cta 151
Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala Leu

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-5          1          5          10
gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc aat 199
Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn
          15          20          25
act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt cag 247
Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln
          30          35          40
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca 295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr
          45          50          55
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta 343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val
          60          65          70          75
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att 391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile
          80          85          90
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat 439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn
          95          100          105
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa 487
Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu
          110          115          120
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt ttttaagagcc 537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp
          125          130
actggcctgt aattgtttga tatatttgta actcttttgta taatgtcaga gactcatggt 597
taatacatag gtgatttgta cctcagagca ttttttaaag gattctttcc aagcgagatt 657
taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt 717
aaatgatcag acagaataat atttttctagt tattatgtgt aagatgaggt gctatttttc 777
tgatgctcat tctgatacaa ctatttttctg tgtcaaatat ctactgtgcc caaatgtact 837
caatttaaatt cattactctg taaaataaat aagcagatga ttcttataaa aaaaaaaaaa 897

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<210> 54
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..634

<220>
 <221> sig_peptide
 <222> 92..139
 <223> Von Heijne matrix
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 seq FLLLTCLFITGTS/VS

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ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc 112
                                Met Pro Pro Phe Leu Leu Leu
                                -15          -10
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat 160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp
          -5          1          5
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac 208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp

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10	15	20	
cac cag ttg gat gag tct	caa ggt cct cct cta	tgt gac aac cat gtg	256
His Gln Leu Asp Glu Ser	Gln Gly Pro Pro Leu	Cys Asp Asn His Val	
25	30	35	
aat ggg gag tgg tac cac	ttc acg ggc atg gcg	gga gat gcc atg cct	304
Asn Gly Glu Trp Tyr His	Phe Thr Gly Met Ala	Gly Asp Ala Met Pro	
40	45	50	55
acc ttc tgc ata cca gaa	aac cac tgt gga acc	cac gca cct gtc tgg	352
Thr Phe Cys Ile Pro Glu	Asn His Cys Gly Thr	His Ala Pro Val Trp	
60	65	70	
ctc aat ggc agc cac ccc	cta gaa ggc gac ggc	att gtg caa cgc cag	400
Leu Asn Gly Ser His Pro	Leu Glu Gly Asp Gly	Ile Val Gln Arg Gln	
75	80	85	
gct tgt gcc agc ttc aat	ggg aac tgc tgt ctc	tgg aac acc acg gtg	448
Ala Cys Ala Ser Phe Asn	Gly Asn Cys Cys Leu	Trp Asn Thr Thr Val	
90	95	100	
gaa gtc aag gct tgc cct	gga ggc tac tat gtg	tat cgt ctg acc aag	496
Glu Val Lys Ala Cys Pro	Gly Tyr Tyr Val Tyr	Arg Leu Thr Lys	
105	110	115	
ccc agc gtc tgc ttc cac	gtc tac tgt ggt cgt	gag tac ctt ccc tgt	544
Pro Ser Val Cys Phe His	Val Tyr Cys Gly Arg	Glu Tyr Leu Pro Cys	
120	125	130	135
gct ctt ttt ctc cac caa	caa ggc cac agg tgg	agt cca aaa gtg ccc	592
Ala Leu Phe Leu His Gln	Gln Gly His Arg Trp	Ser Pro Lys Val Pro	
140	145	150	
aat tat agg ata tgc agt	tac agt ggc aac tat	atc tca atc	634
Asn Tyr Arg Ile Cys Ser	Tyr Ser Gly Asn Tyr	Ile Ser Ile	
155	160	165	
tgaacaacat tgatgtgggg	ctaaagatac tctgatttct	gagatctctt cttagaactt	694
ctgaaaaatt cctgaagaaa	tagaagggga aaggagctat	gactttgatc agttcttttt	754
aattttgtct gaattccatt	caaacaaaac attagaaaat	gaaacattgg gccaggcgca	814
gtggctcatg cctgtaatcc	cagcactttg ggaggctgag	gcgggtggat cacaagatca	874
ggagtttaag accagcctgg	ccaatatggt gaaaccctgt	ctctactaga aatacaaaaa	934
ttagacaggc gtgggtggcag	gcaactgtaa ccccagctac	ccgggagggt gaggcaggag	994
aattgcttga acccgggagg	tggacgttgc ggtcaggcga	aaatcgtgcc attgcactcc	1054
agcctgggtg acagagtgag	actctgatcc aaaaaaaaaa	aaaaaaaa	1101

<210> 55
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..767

<220>
 <221> sig_peptide
 <222> 27..80
 <223> Von Heijne matrix
 score 8.96664802487992
 seq LFCLAVLAASSFS/KA

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agcagaggcc ctacaccac cgaggc	atg ggg ctc cct ggg ctg ttc tgc ttg
	Met Gly Leu Pro Gly Leu Phe Cys Leu
	-15 -10
gcc gtg ctg gct gcc agc agc	ttc tcc aag gca cgg gag gaa gaa att
	101

Ala Val Leu Ala Ala Ser Ser Phe Ser Lys Ala Arg Glu Glu Glu Ile	
acc cct gtg gtc tcc att gcc tac aaa gtc ctg gaa gtt ttc ccc aaa	149
Thr Pro Val Val Ser Ile Ala Tyr Lys Val Leu Glu Val Phe Pro Lys	
ggc cgc tgg gtg ctc ata acc tgc tgt gca ccc cag cca cca ccg ccc	197
Gly Arg Trp Val Leu Ile Thr Cys Cys Ala Pro Gln Pro Pro Pro Pro	
atc acc tat tcc ctc tgt gga acc aag aac atc aag gtg gcc aag aag	245
Ile Thr Tyr Ser Leu Cys Gly Thr Lys Asn Ile Lys Val Ala Lys Lys	
gtg gtg aag acc cac gag ccg gcc tcc ttc aac ctc aac gtc aca ctc	293
Val Val Lys Thr His Glu Pro Ala Ser Phe Asn Leu Asn Val Thr Leu	
aag tcc agt cca gac ctg ctc acc tac ttc tgc cgg gcg tcc tcc acc	341
Lys Ser Ser Pro Asp Leu Leu Thr Tyr Phe Cys Arg Ala Ser Ser Thr	
tca ggt gcc cat gtg gac agt gcc agg cta cag atg cac tgg gag ctg	389
Ser Gly Ala His Val Asp Ser Ala Arg Leu Gln Met His Trp Glu Leu	
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Trp Ser Lys Pro Val Ser Glu Leu Arg Ala Asn Phe Thr Leu Gln Asp	
aga ggg gca ggc ccc agg gtg gag atg atc tgc cag gcg tcc tcg ggc	485
Arg Gly Ala Gly Pro Arg Val Glu Met Ile Cys Gln Ala Ser Ser Gly	
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Ser Pro Pro Ile Thr Asn Ser Leu Ile Gly Lys Asp Gly Gln Val His	
ctg cag cag aga cca tgc cac agg cag cct gcc aac ttc tcc ttc ctg	581
Leu Gln Gln Arg Pro Cys His Arg Gln Pro Ala Asn Phe Ser Phe Leu	
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Pro Ser Gln Thr Ser Asp Trp Phe Trp Cys Gln Ala Ala Asn Asn Ala	
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Asn Val Gln His Ser Ala Leu Thr Val Val Pro Pro Gly Gly Leu Pro	
agg gca ccc acc atc gtg ctg gtt ggc agc ctt gcc tcc act gcg gcc	725
Arg Ala Pro Thr Ile Val Leu Val Gly Ser Leu Ala Ser Thr Ala Ala	
atc acc tcc agg atg ctg ggc tgg acc acg tgg gcc agg tgg	767
Ile Thr Ser Arg Met Leu Gly Trp Thr Trp Ala Arg Trp	
tgaccagaag atggaggact ggcagggtcc cctggagagc cccatccttg ccttgccgct	827
ctacaggagc acccgccgtc tgagtgaaga ggagtttggg gggttcagga tagggaatgg	887
ggagggtcaga ggaacgcaaaag cagcagccat gtagaatgaa ccgtccagag agccaagcac	947
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 Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg
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 Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe
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 Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile
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 Gly Cys Pro Gly Pro
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ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
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gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
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ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
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gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
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Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
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ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct      1009
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Ala	Val	Val	Ser	Ser	Arg	Phe	Glu	Gly	Leu	Ser	Pro	Leu	Gln	Arg	His	

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cgg	ctg	gtc	cac	gca	gcg	ctg	gcc	gag	gag	ctg	gga	ggt	ccg	gtc	cat	461
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Ala	Leu	Ala	Ile	Gln	Ala	Arg	Thr	Pro	Ala	Gln	Trp	Arg	Glu	Asn	Ser	

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Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	Leu	Thr	Trp	Ser	Phe	Phe	
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Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro	Ala	Arg	Leu	Ala	His	Ile	Ala	
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Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	Gly	Thr	Ala	Phe	Leu	Thr	

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cct acc tgt tgc gtg gag cag gcc cag tgg gtg ctg gcc aaa gct cgg      592
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Arg Gly Pro Gln Lys Asp Glu Leu Lys Ser Phe Ile Leu Gln Lys Tyr
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atg atg gtg gat agc gca gag gat cag aag att cac cgg ccc atg gct      784
Met Met Val Asp Ser Ala Glu Asp Gln Lys Ile His Arg Pro Met Ala
    205                      210                      215
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Arg Phe His
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Pro His Ala Leu Arg Pro Leu Leu Leu Leu Pro Leu Val Leu Leu Pro
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gga ggc gag ctg gag acc atc tgc agg tct tgg aat tac ttc cat gcc      242
Gly Gly Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala
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tgt gcc tct cag gtc ctg tca ggc tgt ccg gag gag gca gct gca gtg      290
Cys Ala Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val
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Trp Glu Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn
      60      65      70      75
ttg cac act ctg tgc ggt gcc ccg gtg cat gtt cgg gag cgc ggc aca      386
Leu His Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr
      80      85      90
ggc tcc gaa acc aac cag gag acg ctg cgg gct aca gcg cct gca ctc      434
Gly Ser Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu
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Tyr Leu Leu Arg Pro Leu Ala
      125      130
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Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
      -10      -5      1
gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc aaa aac ctc ggt      149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
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gga aag tca tca ggc aga cgc caa ggc att aag aaa atg gaa ggt cac      197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
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Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp	
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His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala	
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ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat	341
Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His	
70 75 80	
ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt	389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly	
85 90 95	
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Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu	
100 105 110	
ggc acc ttc aaa ctg gta gct atg ctt tgatgtcctg ttgaggccat	484
Gly Thr Phe Lys Leu Val Ala Met Leu	
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Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr	
15 20 25 30	
gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act	417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr	
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Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
65                               70                               75
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Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
80                               85                               90
tca att tca aga cat act ttc cgg gga cta aag tca tta att cac ttg      609
Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
95                               100                              105                              110
agc ctt gca aac aac aat ctc cag aca ctc cca aaa gat att ttc aaa      657
Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
115                              120                              125
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tgt gac tgt aaa ctg aaa tgg cta gtg gaa tgg ctt ggc cac acc aat      753
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
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Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
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Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
195                              200                              205
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 Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
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 Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
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 aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct 294
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Met Gly
ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg 226
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Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
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Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
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Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
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gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg 180
ttcatgggtg gggatatttt ctgcactgc atg gaa tca gaa aga agc aaa agg 233
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Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
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Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
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Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu	
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Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp	
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Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu	
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Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg	
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Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln	
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Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val	
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Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu	
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Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu	
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Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu	
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 Phe Asn Glu Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
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 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr
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 Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu
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 Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile
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 Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr
 75 80 85
 aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac 561
 Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp
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 Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu
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 Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr
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Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met Asn Lys
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tac cat gga cgg aag cta tct atg cag ggc ttc aag gag gca ctt ttc      1041
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gag cgg ccc gaa gtg gtc ctg gac tca gat gct gag gat ttg gag gac      1233
Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu Glu Asp
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ctg tca gag gaa tca gct gat gag tct gct ggt gcc tat gcc tac aaa      1281
Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala Tyr Lys
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ccc atc ggc gcc agc tct gta gat gtg cgc atg atc gac ttt gca cac      1329
Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe Ala His
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Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu Gly Gln
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Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile Val Thr
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Glu Ile Ser Glu Glu Ser Gly Glu
    395
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seq YAAAAGVLAGVES/RQ

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Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser		
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Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu		
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Met	Pro	Glu	Leu	Leu	Val	Phe	Pro	Ala	Gln	Thr	Asp	Leu	His	Glu	His								
															170		175		180				
cca	ctg	tac	cgg	gcc	gga	cac	ctc	att	ctg	cag	gac	agg	gcc	agc	tgt	677							
Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu	Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys								
															185		190		195		200		
ctc	cca	gcc	atg	ctg	ctg	gac	ccc	ccg	cca	ggc	tcc	cat	gtc	atc	gat	725							
Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro	Pro	Pro	Gly	Ser	His	Val	Ile	Asp								
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gcc	tgt	gcc	gcc	cca	ggc	aat	aag	acc	agt	cac	ttg	gct	gct	ctt	ctg	773							
Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys	Thr	Ser	His	Leu	Ala	Ala	Ala	Leu								
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aag	aac	caa	ggg	aag	atc	ttt	gcc	ttt	gac	ctg	gat	gcc	aag	cgg	ctg	821							
Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala	Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu								
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gca	tcc	atg	gcc	acg	ctg	ctg	gcc	cgg	gct	ggc	gtc	tct	tgc	tgt	gaa	869							
Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala	Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu								
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Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala	Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr								
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His Glu Val His Tyr Ile Leu Leu Asp Pro Ser Cys Ser Gly Ser Gly
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Met Pro Ser Arg Gln Leu Glu Glu Pro Gly Ala Gly Thr Pro Ser Pro
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gtg cgt ctg cat gcc ctg gca gct tcc agc agc gag ccc tgt gcc acg      1061
Val Arg Leu His Ala Leu Ala Ala Ser Ser Ser Glu Pro Cys Ala Thr
      315                      320                      325
cgc tca ctt tcc ctt ccc tgc agc ggc tgc tct act cca cgt gct ccc      1109
Arg Ser Leu Ser Leu Pro Cys Ser Gly Ser Ser Thr Pro Arg Ala Pro
      330                      335                      340
tct gcc agg agg aga atg aag acg tgg tgc gag atg cgc tgc agc aga      1157
Ser Ala Arg Arg Arg Met Lys Thr Trp Cys Glu Met Arg Cys Ser Arg
      345                      350                      355                      360
acc cgg gcg cct tca ggc tagctcccg cctgcctgcc tggccccacc      1205
Thr Arg Ala Pro Ser Gly
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gaggcctgag cacgttcccg ggtgccgagc actgcctccg ggccctccct gagaccacac      1265
tcagcagtgg cttcttcggt gctgtaattg aacgggtcga ggtgccaagc tcagcctcac      1325
aggccaaaagc atcagcacca gaacgcacac ccagcccagc cccaaagaga aagaagagac      1385
agcaaaagagc cgcagccggt gcttgacacac cgccttgacac atagcagagg ctccgggctg      1445
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      Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys
      -35                      -30                      -25
ttc acg caa gct gcc cgg act agc ctc tta ctg ctc agg ctc aac gac      158
Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
      -20                      -15                      -10
gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg      206
Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
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gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct      254
Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
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ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag      302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu

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Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser	
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ggg cct aac agc ctc cac tgc ctg ggc tca ctc agg gag cgc ctc att	398
Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile	
60 65 70 75	
att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga	446
Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly	
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cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca	494
His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr	
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Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu	
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Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser	
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175 180 185	
gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg ccc ccc	782
Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro	
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cct aca agg cct gac caa tca gga ttt aca aga ggg aga aga ttg gga	830
Pro Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly	
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Ala Arg Arg	
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gccatccaca gtgcagaaca gcaacatgcc tatgagcagg actttgagac agattatgct	999
gaataaccgca tcttgcattgc ccgtgttggg actgcaagcc aaagggtcat agagctggga	1059
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 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu
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 Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
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 ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg 204
 Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
 1 5 10
 gtg cat ggg ctc ttc gac agc tcg tac agc ttc cgc cac ctg ctg gaa 252
 Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
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 Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
 35 40 45
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 Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly
 50 55 60
 ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg 396
 Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val
 65 70 75
 cat ctc atc tgc tac tcg cag ggg ggc ctt gtg tgc cgg gct ctg ctt 444
 His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu
 80 85 90
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 Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser
 95 100 105 110
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 Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe
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 Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu
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 Phe Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly
 160 165 170
 gtt att act ccc tgg cag tcc agc ttc ttt ggt ttc tat gat gca aat 732
 Val Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn
 175 180 185 190
 gag acc gtc ctg gag atg gag gag caa ctg gtt tat ctg cgg gat tct 780
 Glu Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser
 195 200 205

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      210                      215                      220
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Met Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr
      225                      230                      235
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Glu Thr Cys Ile Glu Pro Trp Leu Ser
      240                      245
cccaggaact cctcgggtcca gagaccaagt ggtggccttg gaaagcagat gtcaggccttt      983
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Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu
      -30                      -25                      -20
ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg      156
Pro Ala Ala Trp Val Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
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ctt gca gcc ccc gcg ccc cac cgc gcg tcc tac aag ccg gtc atc gtg      204
Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
      1                      5                      10
gtg cat ggg ctc ttc gac agc tcg tac agc ttc cgc cac ctg ctg gaa      252
Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
      15                      20                      25                      30
tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc      300
Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
      35                      40                      45
ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg      348
Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly

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65	70	75	
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His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu			
80	85	90	
tct gtc atg gat gat cac aac gtg gat tct ttc atc tcc ctc tcc tct			492
Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser			
95	100	105	110
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Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe			
115	120	125	
ccc acc tcc atg cgg tct aac ctc tat cgg atc tgc tat agc ccc			585
Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro			
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Met Ala Phe Thr Phe Ala Ala		

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Ala	Ile	Trp	His	Ile	Ile	Ala	Phe	Asp	Glu	Leu	Arg	Thr	Asp	Phe	Lys		
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Ser	Pro	Ile	Asp	Gln	Cys	Asn	Pro	Val	His	Ala	Arg	Glu	Arg	Leu	Arg		
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Asn	Ile	Glu	Arg	Ile	Cys	Phe	Leu	Leu	Arg	Lys	Leu	Val	Leu	Pro	Glu		
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Trp	Leu	Thr	Leu	Gly	Leu	Asn	Val	Pro	Leu	Leu	Phe	Tyr	His	Phe	Trp		
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agg	tat	ttc	cac	tgt	cca	gca	gat	agc	tca	gaa	cta	gcc	tac	gac	cca	630	
Arg	Tyr	Phe	His	Cys	Pro	Ala	Asp	Ser	Ser	Glu	Leu	Ala	Tyr	Asp	Pro		
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Trp	Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ser	Phe	Phe	Tyr	Tyr	Leu	Tyr		
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Cys	Met	Ile	Tyr	Thr	Leu	Val	Ser	Ser									
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seq GXLLEPFVHQVGG/HS

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cgcccgagg	atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc	229				
	Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg					
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gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac	277					
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His						
-15 -10 -5 1						
tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc	325					
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val						
5 10 15						
cca agg gaa cat cag ttc tac gag acc ctc cct tct gag atg cgc aaa	373					
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys						
20 25 30						
ttc act ccc cag tac aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat	421					
Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp						
35 40 45						
gaa gac agg aac ttg tgt cta ata gca tat cca ttg aaa ggg gac cat	469					
Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His						
50 55 60 65						
gga att gtg gac att gta gat aat tca gac tgt gaa cca aaa agt aag	517					
Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys						
70 75 80						
ctc cta agg tgg aca aca aac aaa aaa cat cat gtc tta gaa aca gaa	565					
Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu						
85 90 95						
aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg	613					
Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met						
100 105 110						
aag agc cat aag tta gaa gaa gaa ttt gag tgg cta aag aaa tct gaa	661					
Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu						
115 120 125						
gtc ttg tac tac act gta gag aag aag ggg aat ata agt tcc cag ctt	709					
Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu						
130 135 140 145						
aaa cac tat aac cct tgg agc atg aaa tgt cac cag caa cag tta cag	757					
Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln						
150 155 160						
aga atg aag gag aat gca aag cat cgg aac cag tac aaa ttt atc tta	805					
Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu						
165 170 175						
ctg gaa aac ctg act tcc cgc tat gag gtg cct tgt gtc ctt gac ctc	853					
Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu						
180 185 190						
aag atg ggc aca cga caa cat ggt gat gat gct tca gag gag aag gca	901					
Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala						

195					200					205										
gcc	aac	cag	atc	cga	aaa	tgt	cag	cag	agc	aca	tct	gca	gtc	att	ggc		949			
Ala	Asn	Gln	Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly					
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gtg	cgt	gtg	tgt	ggc	atg	cag	gtg	tac	caa	gca	ggc	agt	ggg	cag	ctc		997			
Val	Arg	Val	Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu					
230					235					240										
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Met	Phe	Met	Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe					
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aag	gag	gca	ctt	ttc	cag	ttc	ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt		1093			
Lys	Glu	Ala	Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg					
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Glu	Leu	Leu	Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val					
275					280					285										
ttg	gag	cga	cag	gag	tcc	tac	cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc		1189			
Leu	Glu	Arg	Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val					
290					295					300					305					
att	tat	gat	ggc	aag	gag	cgg	ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct		1237			
Ile	Tyr	Asp	Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala					
310					315					320										
gag	gat	ttg	gag	gac	ctg	tca	gag	gaa	tca	gct	gat	gag	tct	gct	ggc		1285			
Glu	Asp	Leu	Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly					
325					330					335										
gcc	tat	gcc	tac	aaa	ccc	atc	ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg		1333			
Ala	Tyr	Ala	Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met					
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atc	gac	ttt	gca	cac	acc	acc	tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg		1381			
Ile	Asp	Phe	Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val					
355					360					365										
gtg	cat	gag	ggc	cag	gat	gct	ggc	tat	atc	ttc	ggg	ctc	cag	agc	ctg		1429			
Val	His	Glu	Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu					
370					375					380					385					
ata	gac	att	gtc	aca	gag	ata	agt	gag	gag	agt	ggg	gag	tgagcttgct			1478				
Ile	Asp	Ile	Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu								
390					395															
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ctttcaacat		tccacatttg		atgatgatac		ctctttcttc		cctgagtgtg		tatgtttctaa							1718			
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<210> 77
<211> 2027
<212> DNA
<213> Homo sapiens
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<220>
<221> sig_peptide
<222> 48..107
<223> Von Heijne matrix
score 6.64507667657896
seq LLPLLSLLVGAWL/KL
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                                     Met Ala Arg
                                     -20
cat ggg tta ccg ctg ctg ccc ctg ctg tcg ctc ctg gtc ggc gcg tgg      104
His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val Gly Ala Trp
      -15
ctc aag cta gga aat gga cag gct act agc atg gtc caa ctg cag ggt      152
Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln Leu Gln Gly
      1      5      10      15
ggg aga ttc ctg atg gga aca aat tct cca gac agc aga gat ggt gaa      200
Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg Asp Gly Glu
      20      25      30
ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc atc gac ata ttt      248
Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile Asp Ile Phe
      35      40      45
cct gtc acc aac aaa gat ttc agg gat ttt gtc agg gag aaa aag tat      296
Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu Lys Lys Tyr
      50      55      60
cgg aca gaa gct gag atg ttt gga ttg agc ttt gtc ttt gag gac ttt      344
Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe Glu Asp Phe
      65      70      75
gtc tct gat gag ctg aga aac aaa gcc acc cag cca atg aag tct gta      392
Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met Lys Ser Val
      80      85      90      95
ctc tgg tgg ctt cca gtg gaa aag gca ttt tgg agg cag cct gca ggt      440
Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln Pro Ala Gly
      100      105      110
cct ggc tct ggc atc cga gag aga ctg gag cac cca gtg tta cac gtg      488
Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val Leu His Val
      115      120      125
agc tgg aat gac gcc cgt gcc tac tgt gct tgg cgg gga aaa cga ctg      536
Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly Lys Arg Leu
      130      135      140
ccc acg gag gaa gag tgg gag ttt gcc gcc cga ggg ggc ttg aag ggt      584
Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu Lys Gly
      145      150      155
caa gtt tac cca tgg ggg aac tgg ttc cag cca aac cgc acc aac ctg      632
Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg Thr Asn Leu
      160      165      170      175
tgg cag gga aag ttc ccc aag gga gac aaa gct gag gat ggc ttc cat      680
Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp Gly Phe His
      180      185      190
gga gtc tcc cca gtg aat gct ttc ccc gcc cag aac aac tac ggg ctc      728
Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn Tyr Gly Leu
      195      200      205
tat gac ctc ctg ggg aac gtg tgg gag tgg aca gca tca ccg tac cag      776
Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser Pro Tyr Gln
      210      215      220
gct gct gag cag gac atg cgc gtc ctc cgg ggg gca tcc tgg atc gac      824
Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser Trp Ile Asp
      225      230      235
aca gct gat ggc tct gcc aat cac cgg gcc cgg gtc acc acc agg atg      872
Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr Thr Arg Met
      240      245      250      255
ggc aac act cca gat tca gcc tca gac aac ctc ggt ttc cgc tgt gct      920
Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe Arg Cys Ala

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	260	265	270	
gca gac gca ggc cgg ccg cca ggg gag ctg taagcagccg ggtgggtgaca				970
Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu				
	275	280		
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caagctcgag agcttcagcc tcaggaaaga acttcccctt ccctgtctcc catccctctg				1090
tggcaggcgc ctctcaccag ggcaggagag gactcagcct cctgtgtttt ggagaagggg				1150
cccaatgtgt gttgacgatg gctggggggcc aggtgtttct gttagaggcc aagtattatt				1210
gacacaggat tgcaaacaca caaacaattg gaacagagca ctctgaaagg ccatttttta				1270
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aaccagatga tgtactaggt gaagcattgc attgtgggaa tcacaaagca aatagtactc				1570
cagaaagaca aatatcagaa gcttccctatt cttttttttt tttttttttt tttggagaca				1630
gggtctttct ctggtgccc ggctagagtg cactgggtgat cacggctcac tctagccttg				1690
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cccagggtgg tctcgaaact ctggcctcaa gcgactctcc cacctcgacc tcccaaagtg				1870
ctgggattac aggtgtgagc cacctcgctt gggccccctt ctccatatgc ctccaaaaac				1930
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ctcctgcaat tgtgtatctc aaaaaaaaaa aaaaaaa				2027

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 <211> 1880
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 156..512

<220>
 <221> sig_peptide
 <222> 156..206
 <223> Von Heijne matrix
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 seq WLTAVASLLPSPG/NS

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agcgtctcga cggcgctcgg gacctccctc gtccactgct tgagttccag aggtgggtgc	120
ttccctgtcc tgaacttcag agtgcgaggt cataa atg ggt tcc ggc tgg ctt	173
Met Gly Ser Gly Trp Leu	
-15	
act gca gta gcc tcg ctc ctc ccc agc ccc ggt aac tcc gag cta ccc	221
Thr Ala Val Ala Ser Leu Leu Pro Ser Pro Gly Asn Ser Glu Leu Pro	
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gtc cag gcc ctc ggg cgt cgc ggg ggc agg gac tgg gcg cgg aac gag	269
Val Gln Ala Leu Gly Arg Arg Gly Gly Arg Asp Trp Ala Arg Asn Glu	
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gca ggg agg gac ctg gaa aaa cca ccc aga ttg cat tgc agt ggg cga	317
Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg Leu His Cys Ser Gly Arg	
25 30 35	
ggc cgc ctg gag gag ccg gtt ccc cct aac cac ctc ccc gtg ggg ctc	365
Gly Arg Leu Glu Glu Pro Val Pro Pro Asn His Leu Pro Val Gly Leu	
40 45 50	
tcg gtg cgc ggt tcc cag gtg ctc agc tct gct ggg ccc agg agg tgc	413

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Ser Val Arg Gly Ser Gln Val Leu Ser Ser Ala Gly Pro Arg Arg Cys
55                                60                                65
cgc ctc aca ggg acg cgg aac ccc gtg cgt ggc ccc cgc cgg gtg gaa      461
Arg Leu Thr Gly Thr Arg Asn Pro Val Arg Gly Pro Arg Arg Val Glu
70                                75                                80                                85
cag ata gcg cgg ggc ggt ccg gag gct cgt cgc caa gca ggt gac tct      509
Gln Ile Ala Arg Gly Gly Pro Glu Ala Arg Arg Gln Ala Gly Asp Ser
90                                95                                100
tgc tgaaaaagtg gttggaacac ttaaggaaac ccggccccgc ctgttctttc      562
Cys
taggtctttg gagtttggat taatcatttg tgtagcccggt ttggataaac cgaagacttt      622
attaaatcag cgcgtttaac aggaattccg cagtagtata cacattagaa tcttgagtct      682
tggagttgaa catattcaca cagacttgcc ttcttcctgt ttagtttatg ccttggtgtc      742
cgttattgga acgctaagct tgtgggaggt gtttacatcc tactgctcaa ggtcatcgct      802
aaggtgtgat ttttcacaaa aagaatttgc aacctccggc atgaatgact taagggaagt      862
ctaatacccg tttctgattt tttttttttt ttaattttaa agttaatctt tctgggccgg      922
gcgcggtggc tcacgcctgt aatcccagca ctttgggagg ccgaggcgga tcacgaggtc      982
aggagtccga gaccagcctg accaacaatgg tgaaaccccg tctctactaa aaacacaaaa      1042
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ataactggcc tgtactctta catacatgaa agccatcaaa gacaaagact gaagaagaac      1822
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<212> DNA
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<222> 67..183
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gcaatc atg gac tac agc cgt gtc ttt cag ggt gtg ttc ttc acc ttc      108
      Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe
      -35                                -30
aag cat gct ttt gct gat ggt gct tgg gat ctt tca ttt ctc tgt gct      156
Lys His Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala
-25                                -20                                -15                                -10
ctt tgc agt ttc tgc cca atc tca gct gcc tct ggc aga cct tac agg      204

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Leu Cys Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg
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tac ttg gaa ttc tgg aga tta tac ctg tct cct agt tcc atg gaa aat      252
Tyr Leu Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn
      10      15      20
gga gtt caa aaa ttc cac gaa act ttt ttc att gtc ttt ttg ctt ttg      300
Gly Val Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu
      25      30      35
ttt gat atc gag agg aaa gga aaa agt tct gtt tgt cca ttt tgt tac      348
Phe Asp Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr
      40      45      50      55
aga taaggaaaagt gggtttcacaa aggttaagca acttggttcag tgttaccag      401
Arg
caaagagcag aatgattttc aacattcagt ttaaaagtcg gcgggggggca gtgggtcaca      461
cctgtaatat cagcaacttg ggaggccaag gtggtacggc cgcttgaagc caaggagttc      521
aagaccagcc tggtaacat agcaaaacct tgtctttaca aaaagtaaaa aaaaaaaaaa      581
aaa
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<212> DNA
<213> Homo sapiens

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<222> 259..831

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<222> 259..375
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atgacctttc tcacgtgac agtggcctgg gcagcacaca caaggttggt ccaagttggt      180
gggaaaacag acgacacact tgcctgctc aacctggccg catcatggct gtgatgccct      240
ccctccctcc aggctgc atg atg acc atc acc ttc ctg cct tac acg ttt      291
      Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe
      -35      -30
tcg tta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc ttg ttc      339
Ser Leu Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe
      -25      -20      -15
tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att gtg ggg      387
Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly
      -10      -5      1
tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag cgc tct      435
Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser
      5      10      15      20
gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc ctc caa      483
Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln
      25      30      35
ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc ttt gtc      531
Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val
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ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc tat gtc      579

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Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu
70 75 80
ccc tgc gct cac cca gtg gaa gtc ttc tgc ttt gac ctc cac gag cca 675
Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro
85 90 95 100
ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac gcc atc 723
Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile
105 110 115
gtg gcc acg ctt ctc atc ctg gac atc tgc ccc tcc tgc tcc ctt tgg 771
Val Ala Thr Leu Leu Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp
120 125 130
ctg gct gtt gct tcc ttc cag cgt ctg ctc ctc cgc ggc ctc atc tgc 819
Leu Ala Val Ala Ser Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys
135 140 145
ctc ttc gtc tgt tagagcgcgc gtctcgtctc agtcgtcacg tttttgggtt 871
Leu Phe Val Cys
150
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tgctcagcc tccaagtag ttgggattac aagcaccac caccatgccc agctaacttt 1051
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<213> Homo sapiens

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<222> 111..233
<223> Von Heijne matrix
score 5.26415334394122
seq LWFLAQIPSRVAG/SL

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tgcggctgag cgggcctccc atccctctta aaagagttag gcatttagcc atg cct 116
Met Pro
-40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc 164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
-35 -30 -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag 212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
-20 -15 -10
att ccc agt agg gtc gcc ggt agt ctt ctt tct gtc tgt gtg atg agc 260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser

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      -5              1              5
aga gat ggt aac ata aag gac tct ggt gaa gac act cag tcg ggt acc 308
Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser Gly Thr
10              15              20              25
agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg 356
Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg
              30              35              40
cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag 407
Leu Thr Phe Gln Arg Arg Phe
              45
aggaacaagg ggctctggca gctcaaatca attaaccaag atccaattcc ctggagaatt 467
ttaacccct cccactccac ccatcacttg cctggctaac atcagacact ggatcaaccc 527
taaaaaggag tccatccaca gcatccaagg atccatagtg tcccctcaca ctgcagccac 587
caatggaggg tactcccgaa agaaagatgg tggcttcttc tccacctagt gttgacagat 647
ccctgaacta attatagtga aacatactgc ggcccacttc cattaaatag atttgtgcaa 707
aaaaaaaaaa aaa 720

<210> 82
<211> 1029
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..432

<220>
<221> sig_peptide
<222> 223..336
<223> Von Heijne matrix
score 4.17665217008018
seq LVNVLFFFTPLMT/LV

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acatccaaag gagaatagcc ccatgtgaag aatggaatca gtagatgttt ggtcgtgtga 120
ccatatccac tcttaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt 180
cggcttgac cagctaccta tctcagctct ttttgaagc tt atg tcc tcc cca 234
Met Ser Ser Pro
              -35
caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata 282
Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile
              -30              -25              -20
tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg 330
Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu
              -15              -10              -5
atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac 378
Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys Val Thr Lys Asp
              1              5              10
aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg 426
Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp
15              20              25              30
ctg cca taaagatctg gatctcttgg tggggactcc actgaggtga agacctgatt 482
Leu Pro
gtacaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc 542
tgcttttagcc accctgttcc tccattgcca gatgtcccc caggcctcat ttccttctc 602
tgccaccatc cctcttataa tgcactctc ctgcggttct ttggcttgtc ccagcttctg 662
agtttgaatg tctttttttt tttttttttt tttttgkga tcttcaagac tgaaatagta 722

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<220>  
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<222> 769..1272
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ttattttgaac	tgcagtaaag	aaagctggga	tgggctcctc	tagggatact	tccagatccc		120
tgggaggttg	tagccctggc	tcctctttta	atggattttg	tttcaaagac	gatcatctcc		180
gtcttctcgg	atgtcatagt	gccactgatc	atctccagct	cctggccacc	ctgggctttc		240
tccacttttg	cctctatgtt	ttgctttctc	accgtcttag	ccacgatact	tacctctctg		300
ctcagtgtatg	tgacctttgt	ttttgaacca	ggagtggccc	tgaggctcct	taaaaaagag		360
ctgatctttac	tggcttttct	ttgtaaagct	cctgtgctag	atgcagattg	gttcttcccc		420
agttccttgag	ttgttctcga	ctcctttttg	gtggagctgt	gggtggagct	cttgcgagag		480
gagccatgtc	gcttgcccc	tacgttgctg	tacccttttt	cttttttgtc	atctctcgtg		540
tttttatggc	cagatgcgga	ccggtgggaa	gacgctttct	gattcttgtc	ccccgctctc		600
ctgcggtgac	tttcacctgc	cttgcggtga	tgagaacttt	tcctactggg	atgtctgtcc		660
ttcttttctc	ttcttttctc	gttttctatc	cagacttcag	cactgggctg	ggaaactttc		720
tqctttccat	ctccttcact	catqtaqct	tcqctttqca	aggtggag atg	agg ggt		777

-25

106

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Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
75      80      85      90
att gcc aca tct gtt cta ggt cct gtt gct gtt cct gcc act gcc atg      1161
Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala Thr Ala Met
      95      100      105
cca cct gct gtc ctt gct gct cct cct tca gca gcc cct gga gtg ctc      1209
Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
      110      115      120
gtg gat gga gaa gcc gca cta gcc gtt ccg tgg gag gca tgt tgg att      1257
Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
      125      130      135
ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggcttgt      1312
Pro Ser Pro Pro Ala
      140
agagcccagt ctcaactctga tcccccttctc tgtggagctc tgcagcctat accaagggga      1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctccctctctt      1432
atcctggagt taattcaagg gcttataatt agaagaacct gggtcgggtg tgggtggctca      1492
cgcttgtaat cccaacactt tgggaggcca aggagggcag atcgcttgag gccaggagtt      1552
caagaccagc cttgccaca tagcaaaacc ccgactctac taaaaatata aaaaattagc      1612
tggacaggat ggcgcagtc tgtaatccca gctactcagt aggtctgaggt aggagtatcg      1672
cttgaactcg gatggcggag gctgcagtga gccaagactg cgccactcca ctgcactcca      1732
gcctgggcaa cagagtgaga cactgtttaa aaaaaagaaa gaaaaaaaaa aaaaaa      1788

<210> 84
<211> 805
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..527

<220>
<221> sig_peptide
<222> 30..74
<223> Von Heijne matrix
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      seq PLLIICLLPAIEG/KN

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      Met Leu Pro Leu Leu Ile Ile Cys
      -15      -10
ctc ctg cct gcc att gaa ggg aag aac tgc ctc cgc tgc tgg cca gaa      101
Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
      -5      1      5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca      149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
      10      15      20      25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa      197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
      30      35      40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga      245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
      45      50      55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc      293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
      60      65      70

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ttt act gag agg ctg aat aag ata tct gat ggg ctg aag gag aag gac 341
Phe Thr Glu Arg Leu Asn Lys Ile Ser Asp Gly Leu Lys Glu Lys Asp
75 80 85
ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac 389
Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
90 95 100 105
ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg 437
Phe Leu Ser Cys Asn Asp Pro Thr Phe Cys Pro Ala Arg Asn Arg Arg
110 115 120
acc tcc ctg tgg gct gtg agt ctc agc agt gct cta ctc ctg gcc ata 485
Thr Ser Leu Trp Ala Val Ser Leu Ser Ser Ala Leu Leu Leu Ala Ile
125 130 135
gct gga gat gtt tct ttt act ggc aaa gga aga agg agg cag 527
Ala Gly Asp Val Ser Phe Thr Gly Lys Gly Arg Arg Arg Gln
140 145 150
taaagcagga acagggcagc ccgcatgtct tccagaagtg aacagaggcc gcagctacca 587
ccgtcacaaa gtctactcat ctctgggtcc cggtagcccc atccccccat accctccatc 647
ctgggtcctg gggccccaaa gctctgaggc ctaggagact gcgctgtctc gtggtttgcc 707
tactcctaca cctttgtaaa gagtctcttc attaaaaccc ctcttcataa aaaaaaaaaa 767
aaaaaaaaaa aaaaaaaaaa aataaaaaaaaa aaaaaaaaaa 805

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<210> 85
 <211> 814
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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 <221> sig_peptide
 <222> 39..83
 <223> Von Heijne matrix
 score 5.91494342964539
 seq ILMLTFIICGLLT/RV

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Met Asn Ile Leu Met Leu
-15 -10
acc ttc att atc tgt ggg ttg cta act cgg gtg acc aaa ggt agc ttt 104
Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg Val Thr Lys Gly Ser Phe
-5 1 5
gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga 152
Glu Pro Gln Lys Cys Trp Lys Asn Asn Val Gly His Cys Arg Arg Arg
10 15 20
tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca 200
Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu Cys Arg Asn Lys Leu Ser
25 30 35
tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt 248
Cys Cys Ile Ser Ile Ile Ser His Glu Tyr Thr Arg Arg Pro Ala Phe
40 45 50 55
cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac 296
Pro Val Ile His Leu Glu Asp Ile Thr Leu Asp Tyr Ser Asp Val Asp
60 65 70
tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt 344
Ser Phe Thr Gly Ser Pro Val Ser Met Leu Asn Asp Leu Ile Thr Phe

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	75		80		85	
gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct						392
Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro						
	90		95		100	
gag act act atg cca cca tcc gag gcc act act ccc gag act act atg						440
Glu Thr Thr Met Pro Pro Ser Glu Ala Thr Thr Pro Glu Thr Thr Met						
	105		110		115	
cca cca tct gag act gct act tcc gag act atg cca cca cct tct cag						488
Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr Met Pro Pro Pro Ser Gln						
120		125		130	135	
aca gct ctt act cat aat taattaacat ttacttctgg tatggaacaa						536
Thr Ala Leu Thr His Asn						
	140					
ctagaaatac tgctggaaat aatatccaaa gagctgattc taccaatcca atttcaccag						596
gaaaattcca tcagggattg gatgaccatg gggatggaca taattgctac taccaacaca						656
acagccaaga gagttgcctt acaattagaa atgtgtagac agaaatgtat agaagataca						716
aggattctct taattggact taaattcttt atctgtcttc ctccgatgta ctcaaatata						776
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<210> 86						
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<222> 115..429						
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<221> sig_peptide						
<222> 115..210						
<223> Von Heijne matrix						
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seq LVAAMVLLSVVFC/LY						
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atcttaatta ctccatagcag ggataattag gtccctcttt ctcagattac aggc atg						117
					Met	
gca aag atg ttt gat ctc agg acg aag atc atg atc ggc atc gaa agc						165
Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu Ser						
-30		-25		-20		
agc tta ctg gtt gcc gcg atg gtg ctc cta agt gtt gtg ttc tgt ctt						213
Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys Leu						
-15		-10		-5		1
tac ttc aaa gta gct aag gca cta aaa gct gca aag gac cct gat gct						261
Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp Ala						
5		10		15		
gtg gct gta aaa aat cac aac cca gac aag gtg tgt tgg gcc acg aac						309
Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr Asn						
20		25		30		
agc cag gcc aaa gcc acc acc atg gag tct tgt cca tct ctc cag tgc						357
Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln Cys						
35		40		45		
tgt gaa ggt tgt aga atg cat gcc agt tct gat tcc ctg cca cct tgc						405
Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro Cys						
50		55		60		65
tgt tgt gac ata aat gag ggc ctc tgacttggga aagctgggca caaaaatctt						459

Cys Cys Asp Ile Asn Glu Gly Leu

70

catgagcaat atttctttct taatagaatg ttttattatt caagtcaagt tctagagtgt	519
ttacatacta ttatataatg tacagtgtta ttttctgtac ttctgaataa atgtgcaata	579
ttgcaaaaaa aaaaaaaaaa	598

<210> 87
 <211> 699
 <212> DNA
 <213> Homo sapiens

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 <222> 332..574

<220>
 <221> sig_peptide
 <222> 332..412
 <223> Von Heijne matrix
 score 7.96491294552426
 seq ILGLFCCLPLAIP/AV

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gcagaaagga gagtctcgct ctgtcaccca ggctggagtg cagtggcagg atcttggtc	180
acttcaacct ccacctcccg agttctgcct cagcctccca agtagctggg attacaggtc	240
cagtcaactc acgcttgag agtccaatta acaagagcaa gttctggtag aaagaaggtg	300
actttattcc agagctcagg tgtttgaact g atg tct gat gag gat gaa tcc	352
Met Ser Asp Glu Asp Glu Ser	

-25

agc gac tac ctc tgc ctg tcc atc ctg ggc ctc ttc tgt tgc ctt ccc	400
Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Cys Leu Pro	
-20 -15 -10 -5	
cta gcc atc cca gcc gtg atc ttt tct tgc ctg aca aag aac tac aat	448
Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn	
1 5 10	
aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac	496
Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr	
15 20 25	
tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg	544
Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu	
30 35 40	
tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt	594
Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu	
45 50	
gaacaaacca ccaaatatac accacagtgc aatttaaaaa aaaaaaaaaa aaaaaaaaaa	654
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa	699

<210> 88
 <211> 905
 <212> DNA
 <213> Homo sapiens

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 <222> 133..213
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 gccagtttcc tcccagggcc attgttacca cctgatcatt tgagtttttag tttctctagc 120
 agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly
 -25 -20 -15
 agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219
 Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val
 -10 -5 1
 ttc cct caa cta cct cca aaa ccg ttg aat ata ttc ttt gct gtc tgc 267
 Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys
 5 10 15
 atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315
 Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln
 20 25 30
 gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363
 Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe
 35 40 45 50
 tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411
 Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val
 55 60 65
 gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467
 Gly Arg
 aggacagtga gtaattttttg gataaggtat gctgaagaat ctctctgcaga agtctgatac 527
 atgattttca tgttaattgt aaatgttaaat tccctcttgc aaggagagaca tatcctagat 587
 cactttgctt tttctttaag gagctgatgt tgcacctaata cattccaacc cttaaagcta 647
 aaacagcaca aaaaaatttc actttttgaaa tgaaattttt ataattgtat ggcaaaaaggc 707
 tatgtaaaaa caaatcttgc atcttaagac aaatattctt ttattttctgt taaactgaat 767
 atacaattgt tccctaggca accaactttt gcttataact acaatttaat ttcacgttga 827
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<210> 89
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 113..364

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 <221> sig_peptide
 <222> 113..172
 <223> Von Heijne matrix
 score 4.37180298395146
 seq SLLLSLPPHQGLT/FS

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 tcgctggacc ctagaaaagc caccacgacc tgtgggcat gatgctaccc ca atg gct 118

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Met Ala
-20
gct gct gct gtt cct tct ctt ctt ctt tct ctt cct cct cac cag ggg      166
Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His Gln Gly
-15 -10 -5
ctc act ttc tcc aac aaa ata caa cct ttt gga gct caa gga gtc ttg      214
Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly Val Leu
1 5 10
cat ccg gaa cca gga ctg cga gac tgg ctg ctg cca acg tgc tcc aga      262
His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys Ser Arg
15 20 25 30
caa ttg cga gtc gca ctg ccg gag aag ggg tcc gag ggc agt ctg tgt      310
Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser Leu Cys
35 40 45
caa acg cag ctg cca gct act cca tgc ttc ctg cct tcg aat acg gtg      358
Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val
50 55 60
aga acg tgaagtcag agctgctgct aaggcatgtg gcaaccttga agagaaggtc      414
Arg Thr
aagagctacc agccacaaaa agaatgccag cacttctgt gtctttgctt tggattcatg      474
agaaatatac gttcctatgt gcttcaaaaa aaaaaaaaaa      514

<210> 90
<211> 518
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..380

<220>
<221> sig_peptide
<222> 9..104
<223> Von Heijne matrix
score 4.73369226787171
seq AVFAVLFFVFFLFA/ML

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Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly
-30 -25 -20
gtt cct tgg ctc tat gct gtg ttt gct gtg ctt ttt gta ttt ttt ctt      98
Val Pro Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu
-15 -10 -5
ttt gcc atg tta tct ccc ttt tta ctt gag ata gac cag cac ata aag      146
Phe Ala Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys
1 5 10
aaa ttc ttg atc aga tgc agg tat tct ctg cat aac act gtg cat aag      194
Lys Phe Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys
15 20 25 30
gac aaa aaa aac agt gag ata aag atg gac cat cta gaa agg cca ggc      242
Asp Lys Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly
35 40 45
tgt cca ctg gag tca cca agg aga gga gtt ctg gga ggg aag aaa aat      290
Cys Pro Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn
50 55 60
ggg atg gga aac gac cca tta cta ttt gtg aaa gtg aca aaa gaa ccc      338

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Gly Met Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro
65 70 75
agg gat tct gag gct gaa atc tat acc cct ggg cct tca gtt 380
Arg Asp Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
80 85 90
tgagagtcatt ttagcctata tggaattacc tgtgacatta cattccagag agatgagaaa 440
ttctgagacc cttattatcg atgtttatat tgaaaaaatg gtaataaata ttttgagact 500
cccaaaaaaa aaaaaaaa 518

<210> 91
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<212> DNA
<213> Homo sapiens

<220>
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<222> 155..340

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<222> 155..292
<223> Von Heijne matrix
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seq AVLLLLILFAIVFG/LL

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gacccagaac agctaccagc agaatcagat tctc atg gac caa ctg gta ttc aaa 175
Met Asp Gln Leu Val Phe Lys
-45 -40
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Glu Thr Ile Trp Asn Asp Ala Phe Trp Gln Asn Pro Trp Asp Gln Gly
-35 -30 -25
ggc ctg gca gtg att atc tta ttc atc acc gct gtc ctg ctt ctc atc 271
Gly Leu Ala Val Ile Ile Leu Phe Ile Thr Ala Val Leu Leu Leu Ile
-20 -15 -10
tta ttt gcc atc gtg ttt ggt tta ctc act tcc aca gaa aac act cag 319
Leu Phe Ala Ile Val Phe Gly Leu Leu Thr Ser Thr Glu Asn Thr Gln
-5 1 5
tgt gaa gcg ggt gaa gag gag tgacctgact tgctggggac tgagatggca 370
Cys Glu Ala Gly Glu Glu Glu
10 15
gcagggggagg cgagctgacc tgccccatt ccagtggttg gccccttcgc ggttcctctt 430
ggctcagggg ccaagccctg gtgtcttctt ttcccaccag gaaaaagtct agtaaaatac 490
tgtatctggc ttaggggttg tcagactagt aagatgggga ggctgggtctg agaccaattc 550
tggtccttg accctattgt ttttagggtt ccccgaccag aaccctaaaa gcacatggag 610
aggatggctc cactgcctca ggtggaagga gctatggcta acaagggttct ctaacaggct 670
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<210> 92
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<222> 185..634

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seq SLLFICFFGESFC/IC

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agctaattta gctatttttaa aatagctaaa ttttagctac ttttttttca attgacaaaag 180
aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
-20 -15 -10
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Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
-5 1 5
aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325
Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly
10 15 20
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Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu
25 30 35 40
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Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln
45 50 55
aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469
Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu
60 65 70
gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517
Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala
75 80 85
acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565
Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His
90 95 100
cct tcc tct aag aaa att aag cac tgc aaa tta aag aag aag agt aaa 613
Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys
105 110 115 120
gaa gaa gga gcc aga aga tac taaataaatg catatgcaaa tgtagcttag 664
Glu Glu Gly Ala Arg Arg Tyr
125
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aaaaaaaaaa aaa 737

<210> 93
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<222> 53...91

<223> Von Heijne matrix

score 4.95353272042967

seq MLLGRLTSQLLRA/VP

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Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp Ala Gly
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Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys
10 15 20
ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct 202
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser
25 30 35
ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg 250
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val Pro Arg
40 45 50
aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc tgc ttc 298
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe
55 60 65
ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa 346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln
70 75 80 85
tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg 394
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly
90 95 100
gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg 442
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu
105 110 115
aag atc cgc cgg cgg aag atg aac cac cac aag tac cgg aag ctg gtg 490
Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val
120 125 130
aag aag acg cgg ttc ctg cgg agg aag gtc cag gag gga cgc ctg aga 538
Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg
135 140 145
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag 586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys
150 155 160 165
gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac 634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr
170 175 180
ctg cgg ggc aaa tgagtctggc gccgcccttc ccgccggttg ctgctgtgat 686
Leu Arg Gly Lys
185
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<210> 94

<211> 582

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 247...510

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 <222> 247..318
 <223> Von Heijne matrix
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 cttgccctga acagttccaa atgccaaagaa ctggcgaatt actactttgg ttccaatggg 180
 tgttccaaaa ggatcatcaa gcttcaggag ctttctgacc ttgaagaaag ggaaaatgaa 240
 gatagc atg gtg cca ctt ccg aag caa agc ctg aag ttc ttc tgt gct 288
 Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala
 -20 -15
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 Leu Glu Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly
 -10 -5 1 5
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 Leu Val Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe
 10 15 20
 ctt atg aaa agg aag aca gcc cag aag ctt gct att cag aag gct ttg 432
 Leu Met Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu
 25 30 35
 tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc 480
 Ser Asp Ala Phe Gln Lys Leu Ile Val Val Leu Gly Lys Thr Val
 40 45 50
 ttg atc atc ctt gaa gta ctt cag ttt cag taagcaaata aactcatttt 530
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<210> 95
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 <222> 143..277
 <223> Von Heijne matrix
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 seq VLVDLAILGQAYA/FA

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 cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172
 Met Val Leu Met Trp Thr Ser Gly Asp Ala
 -45 -40
 ttc aag acg gcc tac ttc ctg ctg aag ggt gcc cct ctg cag ttc tcc 220
 Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
 -35 -30 -25 -20
 gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag 268

Val	Cys	Gly	Leu	Leu	Gln	Val	Leu	Val	Asp	Leu	Ala	Ile	Leu	Gly	Gln	
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gcc	tac	gcc	ttc	gcc	cca	ccc	cca	gaa	gcc	ggc	gcc	cca	cgc	cgt	gca	316
Ala	Tyr	Ala	Phe	Ala	Pro	Pro	Pro	Glu	Ala	Gly	Ala	Pro	Arg	Arg	Ala	
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ccc	cac	tgg	cac	caa	ggc	cct	ctg	aca	gtg	ggg	agg	acg	agg	atg	tgg	364
Pro	His	Trp	His	Gln	Gly	Pro	Leu	Thr	Val	Gly	Arg	Thr	Arg	Met	Trp	
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gac	cgc	cag	ccg	cgg	gca	ctg	gtg	ggc	cct	gac	ctc	ccc	gcg	ggg	agg	412
Asp	Arg	Gln	Pro	Arg	Ala	Leu	Val	Gly	Pro	Asp	Leu	Pro	Ala	Gly	Arg	
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gtg	ggt	gcc	gtg	gcc	cct	gca	ggt	gtg	gca	gag	atg	ggg	cac	ggg	cat	460
Val	Gly	Ala	Val	Ala	Pro	Ala	Gly	Val	Ala	Glu	Met	Gly	His	Gly	His	
			50					55					60			
tgg	ggt	ctc	cat	cag	cct	ctg	tgg	ggt	gtc	tca	ggg	tgg	gca	gtg	ggg	508
Trp	Gly	Leu	His	Gln	Pro	Leu	Trp	Gly	Val	Ser	Gly	Trp	Ala	Val	Gly	
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Val	Gly	Leu	Gly	Arg	Cys	Leu	Cys	Ser	Ala	Gly	Thr	Ala	Arg	Val	Asp	
		80				85					90					
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Leu	Ala	Pro	Arg	Val	Leu	Asp	Val	Phe	Arg	Met	Thr					
	95				100						105					
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gagttttcct	cggaaacact	cttgaatgtc	tgagtgaggg	tcctgcttag	ctctttggcc											1742
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<210> 96
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 33..458

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 <222> 33..89

<223> Von Heijne matrix
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seq SVFLLMVNGQVES/AQ

<400> 96

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Val Phe Leu Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro
                                -10                                -5                                1
gag tat gat gac ttc tac tgc aag tac tgc ttt gtg tac ggc cag gac      149
Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr Cys Phe Val Tyr Gly Gln Asp
5                                10                                15                                20
tgg gcc ccc aca gcg ggt ctg gag gag ggg atc tca cag atc aca tcc      197
Trp Ala Pro Thr Ala Gly Leu Glu Glu Gly Ile Ser Gln Ile Thr Ser
                                25                                30                                35
aag agc caa gat gtg cgg caa gca ctg gtg tgg aac ttc ccc att gat      245
Lys Ser Gln Asp Val Arg Gln Ala Leu Val Trp Asn Phe Pro Ile Asp
                                40                                45                                50
gtc acc ttt aaa agc acc aac ccc tac ggc tgg cca cag atc gtg ctc      293
Val Thr Phe Lys Ser Thr Asn Pro Tyr Gly Trp Pro Gln Ile Val Leu
                                55                                60                                65
agc gtg tat gga cca gat gtg ttc ggg aac gat gtg gtt cga ggc tat      341
Ser Val Tyr Gly Pro Asp Val Phe Gly Asn Asp Val Val Arg Gly Tyr
                                70                                75                                80
ggg gcc gtg cac gtg ccc ttc tca cct ggc cgg cac aaa agg acc atc      389
Gly Ala Val His Val Pro Phe Ser Pro Gly Arg His Lys Arg Thr Ile
85                                90                                95                                100
ccc atg ttt gtc cca gaa tct acg tct aaa ctg cag aag ttt aca aga      437
Pro Met Phe Val Pro Glu Ser Thr Ser Lys Leu Gln Lys Phe Thr Arg
                                105                                110                                115
tct gca agc tgc tcc acc cac tgaggacaaa tagaaacagg tcccctggga      488
Ser Ala Ser Cys Ser Thr His
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<222> 1..81
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<400> 97
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Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn His
-10 -5 1 5
gca ccc aac ttc tcc agc cac ggc tca tgc cgc cgt cgc cag cgg scc 144
Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg Xaa
10 15 20
gac atg aca agg cgc tgc atg ccc gct agg cca ggt ttc ccc tca tcc 192
Asp Met Thr Arg Cys Met Pro Ala Arg Pro Gly Phe Pro Ser Ser
25 30 35
cca gcc ccg ggg tgc tgc ccc ccg cgc tgc cat ctg aga ccc ggt agt 240
Pro Ala Pro Gly Ser Ser Pro Pro Arg Cys His Leu Arg Pro Gly Ser
40 45 50
acc gcc cat gct gca gcg gga aag aga aca gag agt cct ggg gac agg 288
Thr Ala His Ala Ala Ala Gly Lys Arg Thr Glu Ser Pro Gly Asp Arg
55 60 65
tac cgt gca gag ggc ttg aga agg ggc cgg gtc gcg ggg gca agg gta 336
Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val Ala Gly Ala Arg Val
70 75 80 85
tgaggggagg gctgcagacc gccgctcttc cagttcccgc catcctccgc gagctcaggc 396
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<210> 98
<211> 661
<212> DNA
<213> Homo sapiens

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<222> 174..443

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<222> 174..269
<223> Von Heijne matrix
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gcatacctcac ctcagaccat cagttgggta ggccaacagc tcaccatcaa ttc atg 176
Met
ccc tgc cta gac caa cag ctc act gtt cat gcc cta ccc tgc cct gcc 224
Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro Ala
-30 -25 -20
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Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala Gln

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Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu Val
      5          10          15
ctg caa cac cag gaa tgc cag gat gat tta gcc acc tcc tca ctt gtc      368
Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu Val
      20          25          30
tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt cga tgc aag cac caa      416
Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His Gln
      35          40          45
agc atc act gtt gct gac act aac aag tagtgccaag ggattgcctt      463
Ser Ile Thr Val Ala Asp Thr Asn Lys
      50          55
taaggaagat caggagcggg acatctgggtg gcaaagaaaa tcttttctaag agccccattc      523
tagtgaccac cttcaacctc ctcatagcag gagagtttgg gagtagggga cttaggatgt      583
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<210> 99
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<212> DNA
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<222> 282..521

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<221> sig_peptide
<222> 282..386
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cctttggcaa ttccagcctt ctgtggaaag gccagtagaa agcattgatt tattcacctc      240
tacaggaatc agactcagcc tcttttggtt ttcagtgaag t atg cct ttt caa ttt      296
                                     Met Pro Phe Gln Phe
                                     -35
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att      344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile
-30          -25          -20          -15
gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag      392
Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu
      -10          -5          1
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg      440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu
      5          10          15
aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca      488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro
      20          25          30
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg      541
Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
      35          40          45
tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct ggtaaacaaa      601

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647

<210> 100

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<212> DNA

<213> Homo sapiens

<220>

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<222> 251..643

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<221> sig_peptide

<222> 251..295

<223> Von Heijne matrix

score 3.74215118492367

seq LLMFTQLLLCGFL/YV

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atctcagtgt gccccgttcg agacctctcc accaacacct tctgatcttg cgatttgctc 120

ttcttgactt taattagtat ctaggaaagt ctaaactttg gacctacctc tttttttgat 180

actcattttt gtacttttgc tctctgggat tggtttctta aagaatctgg atccttttta 240

atatgtcaaa atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga 289

Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly

-15

-10

-5

ttt tta tat gtt cgg gtt gat gga tcg cgt ctt cgc cag gag gac ttt 337

Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe

1

5

10

ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc 385

Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly

15

20

25

30

gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc 433

Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr

35

40

45

att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat 481

Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp

50

55

60

ccc ccg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg 529

Pro Arg Ser His Arg Met Leu Pro Ser Gly Ser Leu Phe Phe Leu

65

70

75

cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt 577

Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val

80

85

90

tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct 625

Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser

95

100

105

110

ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta 673

Leu Glu Val Ala Cys Lys

115

cttttattta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc 733

aatcaacaca ctgcataatt ttacttggtc ttcttcagag aagtctggtc aagatagtat 793

caagccaggg tggtgtagta agtttggtta tatgaaatca agatgaccaa tatgttatta 853

taagaaagca ggccgggcgc ggtggctcac gcctgtaatc ccagcacttt gggagggcga 913

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 seq PSLIAGLFGVCLA/GY

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 gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca 178
 atg gac ctg atc ggt ttt ggt tat gca gcc ctc gtg aca ttt gga agc 226
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 att ttt gga tat aag cgg aga ggt ggt gtt ccg tct ttg att gct ggt 274
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 ctt ttt gtt gga tgt ttg gcc gcc tat gga gct tac cgt gtc tcc aat 322
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct 370
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct 418
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 ggt ttg gtt gca ggt tta agc ctc atg atg atc ctg aga ctt gtc ttg 466
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515
 Leu Leu Leu
 60
 tgctgtaatg ggcagagcat attttttttg tattttaaag ataaacttca atatggaatg 575
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 ctaaagcaaa aatttttaact gttttcta atgtcaagcac tattttcatt aaaagtgtct 695
 aatgaatcat gatatactct tccatttggt gtgtctat tttatatatt tggatttttt 755
 tgaaaattcc aaatactcat gtctcaagta agcttaaaact acaacttgct acataaagga 815
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 tttaaaaaat tttattctta gcacactggt atgtcctaac tgaatgtatt cagtattcaa 995
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 aaaa' 1059

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 <213> Homo sapiens

<220>
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<222> 34..327

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<221> sig_peptide

<222> 34..162

<223> Von Heijne matrix

score 5.69273078757386

seq LGDALLFLRPAGS/CA

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Met Cys Glu Thr Leu Leu Thr

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agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt 102
Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly

-35

-30

-25

gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt 150
Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg

-20

-15

-10

-5

cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc 198
Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala

1

5

10

ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg 246
Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu

15

20

25

aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca 294
Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser

30

35

40

ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg 347
Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr

45

50

55

gcacccctgaa aacggccttc cttgtgtgta cattatttgc aacaagcaac aagtttataa 407
gcacttttggg aaaattgcat gtgagggtta aaatattaaa gtcagtgcgt caacttgaaa 467

taaatgatga gttattgatt actgctaaag aaaaaaaaaa aaaaaaaa 514

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 303..953

<220>

<221> sig_peptide

<222> 303..359

<223> Von Heijne matrix

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ttatctctaa cggttgaaaa cgatggagct aacacccatt atggagatta accacttttc 120

atcaggtttt taacttaagt cgtgaggat aacacgggtg acacaagatt cattttattt 180

tcacaccat gggacgtatc ctgttggtga gttctctggg tcagacctct gaagacttct 240

cagatggatc ctagtctctg ggcttgccct gaaattactc gctgctcagg gagagagttg 300

aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tgc 347

Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser																	395
-15 -10 -5																	
ctc	tgt	tgt	tcc	agc	tat	gtc	ccc	tct	gtt	gct	cca	act	gca	gct	cat		
Leu	Cys	Cys	Ser	Ser	Tyr	Val	Pro	Ser	Val	Ala	Pro	Thr	Ala	Ala	His		
1 5 10																	443
tct	gtt	aga	gtt	cct	cat	tca	gct	ggg	cac	tgt	ggc	cag	agg	gtg	ttg		
Ser	Val	Arg	Val	Pro	His	Ser	Ala	Gly	His	Cys	Gly	Gln	Arg	Val	Leu	491	
15 20 25																	
gcc	tgc	tcc	ctt	cct	caa	gta	ttc	tta	aag	cca	tgg	att	ttt	gtg	gag	539	
Ala	Cys	Ser	Leu	Pro	Gln	Val	Phe	Leu	Lys	Pro	Trp	Ile	Phe	Val	Glu		
30 35 40																	587
cat	ttt	tct	tcc	tgg	ctc	tcc	ctt	gag	tta	ttt	tcc	ttt	ctt	cgc	tat		
His	Phe	Ser	Ser	Trp	Leu	Ser	Leu	Glu	Leu	Phe	Ser	Phe	Leu	Arg	Tyr		
45 50 55 60																	635
ctt	ggg	act	ctt	ctt	tgt	gct	tgc	gga	cat	cgg	ttg	aga	gaa	gga	cga		
Leu	Gly	Thr	Leu	Leu	Cys	Ala	Cys	Gly	His	Arg	Leu	Arg	Glu	Gly	Arg		
65 70 75																	683
ctt	ctt	cct	tgt	ctc	ctt	ggg	gtt	ggc	tgc	tgg	ttg	ctc	ttc	aac	aac		
Leu	Leu	Pro	Cys	Leu	Leu	Gly	Val	Gly	Ser	Trp	Leu	Leu	Phe	Asn	Asn		
80 85 90																	731
tgg	act	gga	ggc	tct	tgg	ttt	tct	ctt	cat	ctt	caa	caa	gtc	agt	ctc		
Trp	Thr	Gly	Gly	Ser	Trp	Phe	Ser	Leu	His	Leu	Gln	Gln	Val	Ser	Leu		
95 100 105																	779
tct	caa	ggg	tct	cac	gtt	gca	gca	ttc	tta	cca	gag	gcc	att	ggg	cct		
Ser	Gln	Gly	Ser	His	Val	Ala	Ala	Phe	Leu	Pro	Glu	Ala	Ile	Gly	Pro		
110 115 120																	827
gga	gtt	cca	gtt	cca	gtg	tct	gga	gag	tcc	acc	tca	gct	cag	caa	tct		
Gly	Val	Pro	Val	Pro	Val	Ser	Gly	Glu	Ser	Thr	Ser	Ala	Gln	Gln	Ser		
125 130 135 140																	875
cat	gcc	ggg	tgg	caa	ttg	tca	gca	gaa	gcc	gat	gcc	tgc	cca	tca	gtt		
His	Ala	Gly	Trp	Gln	Leu	Ser	Ala	Glu	Ala	Asp	Ala	Cys	Pro	Ser	Val		
145 150 155																	923
ctt	tac	tct	gag	gtg	tta	gag	tgg	aat	aaa	aat	ata	aat	act	tat	act		
Leu	Tyr	Ser	Glu	Val	Leu	Glu	Trp	Asn	Lys	Asn	Ile	Asn	Thr	Tyr	Thr		
160 165 170																	973
agt	ttt	cat	gac	ttc	tgc	tta	ata	ttg	ggg	att	ttt	ktt	gtt	ttg	ttt		
Ser	Phe	His	Asp	Phe	Cys	Leu	Ile	Leu	Gly	Ile	Phe	Xaa	Val	Leu	Phe		
175 180 185																	1033
tgt	ttt	ggc	ggg	gat	agg	ctt	acc	tta	cat	taa	acc	aggc	cttagc	ctttt			
Cys	Phe	Gly	Gly	Asp	Arg	Leu	Thr	Leu	His								
190 195																	1093
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200 205																	1153
agggtccacac	ctggggctgt	ttgtttttcta	cgtttacctc	aacataaggt	accttatcat												
210 215																	1158
gtgcagcctt	catctcctga	tccaaaataa	aataaaatgc	cacaggtcaa	aaaaaaaaaa												
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aaaaa																	

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<210> 104
<211> 1563
<212> DNA
<213> Homo sapiens
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<222> 97..645
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<221> sig_peptide
<222> 97..156
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<223> Von Heijne matrix
 score 8.42885652997473
 seq AVVGCLLVPPAEA/NK

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<221> misc_feature

<222> 972

<223> n=a, g, c or t

<400> 104

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gtgtccggct ttgctggccc agcaagcctg ataagc atg aag ctc tta tct ttg      114
                                     Met Lys Leu Leu Ser Leu
                                     -20                               -15

gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag      162
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                                     -10                               1
agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac      210
Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                                     5                               10                               15
atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac      258
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                                     20                               25                               30
tgc ctg cac gtg gtg gag ccc atg cca gtg cct ggc cat gac gtg gag      306
Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
35                               40                               45                               50
gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc      354
Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
                                     55                               60                               65
acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg      402
Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
                                     70                               75                               80
ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag      450
Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
                                     85                               90                               95
ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat      498
Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
100                               105                               110
gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca      546
Ala Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
115                               120                               125                               130
aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg      594
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
                                     135                               140                               145
cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc      642
Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
                                     150                               155                               160
agc tagatgggct ggtgtggttg ggtcaaggcc ccaacacccat ggctgccagc      695
Ser

ttccaggctg gacaaagcag ggggctactt ctcccttccc tcggttccag tcttcccttt      755
aaaagcctgt ggcatttttc ctcttctccc ctaacttttag aaatgttgta cttggctatt      815
ttgattaggg aagaggggatg tgggtctctga tctctgttgt cttcttgggt ctttgggggt      875
gaagggaggg ggaaggcagg cccasaaggg aatggagaca ttcgaggcgg cctcaggagt      935
ggatgcgac ttgtctctcc tkggcctccc actcttngcc gccttccagc tctgagtctt      995
gggaatgttg ttacccttg aagataaagy ctgggtcttc aggaactcag tgtctgggag      1055
gaaagcatgg cccagcattc agcatgtgtt ctttctgca gtggttctta tcaccacctc      1115
cctcccagcc ccagcgctc agccccagcc ccagctccag ccctgaggac agctctgatg      1175
ggagagctgg gccccctgag cccactgggt cttcagggtg cactggaagc tgggtgttcgc      1235

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tgteccctgt gcacttctcg cactggggca tggagtcccc atgcatactc tgctgcccgt 1295
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gcccctgtac ttgggttgcc tcttgccct gaacttcggt gtaccagtgc atggagagaa 1475
aattttgtcc tcttgtctta gagttgtgtg taaatcaagg aagccatcat taaattgttt 1535
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<210> 105
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 80..118
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 seq MLVLRSAIETRALA/SR

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          Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
          -10          -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
          1          5          10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15          20          25          30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
          35          40          45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
          50          55          60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
65          70          75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
80          85          90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
95          100          105          110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
115          120          125
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
130          135          140
ggt ggg cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
145          150          155

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cat gtc aat cta ggc tac aca aaa cta gtt gga gtg ttc cac aca gag      640
His Val Asn Leu Gly Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu
      160      165      170
tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca      688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Trp Asn Glu Ser Ala
      175      180      185      190
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt      736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val
      195      200      205
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat      784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Asn
      210      215      220
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagtttttcta      830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys
      225      230
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattgg tgettaaatt      890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gtttaatttgc tatgtttctt      950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctgtttac      1010
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tttcacatta gttatttgtc acttacttgg aaaatgatgc tgttaggtcc tgggtattaaa      1430
aatctagaaa agacttggtg gtttatgtgc tgaaatgtct ttatttataa ttaattttaa      1490
ctactattta ctttatttcg gatcctgttt aacaaagata cttgagacat ccatttggtt      1550
taatgaaatc tgtatggata tggaaatgct tgccttaata aaagcctaca tatacaaaaa      1610
aaaaaaaaa a      1621

<210> 106
<211> 557
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..388

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<222> 77..217
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      Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro
      -45      -40
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt      160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe
      -35      -30      -25      -20
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt      208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys
      -15      -10      -5
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag      256

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Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu
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ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg      304
Gly Arg Tyr Thr Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp
      15           20           25
ccc acc aga gac aag aac agg atg ata agc aat gga atg gca ttg aac      352
Pro Thr Arg Asp Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn
      30           35           40           45
tct cct gct gaa gga ctt gca ttt caa tgt aga ttc tgaggctggg      398
Ser Pro Ala Glu Leu Ala Phe Gln Cys Arg Phe
      50           55
tgaaaacttc tctgtcacct ttactacagc attctcaccc atttatatatt ctttcccctt      458
ctacatctct attactgttg cactatgtta tgcattacac catggcaaaa ttaatcaatt      518
aatacaataa aagcttaatt ttaaaaaaaaa aaaaaaaaaa      557

<210> 107
<211> 600
<212> DNA
<213> Homo sapiens

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<222> 139..513

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<222> 139..201
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      score 5.86857787719223
      seq IVMGVQVVGRAFA/RA

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tgacccgccg accacgcttg atccccggcc gcggggccag gaagtcggag tttgagcccc      120
ggaggcagag cggctgcc atg gcc aag tac ctg gcc cag atc att gtg atg      171
      Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met
      -20           -15
ggc gtg cag gtg gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag      219
Gly Val Gln Val Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu
-10           -5           1           5
ttt gca gcc agc cgg gcc gca gct gat gcc cga gga cgc gct gga cac      267
Phe Ala Ala Ser Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His
      10           15           20
cgg tct gca gcc gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca      315
Arg Ser Ala Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala
      25           30           35
cag cag att ctc aac gtg tcc aag ctg agc cct gag gag gtc cag aag      363
Gln Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys
      40           45           50
aac tat gaa cac tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc      411
Asn Tyr Glu His Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser
      55           60           65           70
ttc tac ctg cag tca aag gtg gtc cgc gca aag gag cgc ctg gat gag      459
Phe Tyr Leu Gln Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu
      75           80           85
gaa ctc aaa atc cag gcc cag gag gac aga gaa aaa ggg cag atg ccc      507
Glu Leu Lys Ile Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro
      90           95           100

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cat acg tgactgctcg gctccccccg cccaccccg cgctctaatt ttatagcttg 563
 His Thr
 gtaataaaatt tcttttctac aaaaaaaaaa aaaaaaa 600

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 <223> Von Heijne matrix
 score 5.03543461931947
 seq ITLLGLAVNVVT/LV

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 Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu
 -15 -10
 gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg 161
 Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr
 -5 1 5
 gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga 209
 Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly
 10 15 20 25
 ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga 257
 Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg
 30 35 40
 aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt 305
 Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys
 45 50 55
 gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct 353
 Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala
 60 65 70
 cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg 401
 Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly
 75 80 85
 atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg 449
 Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met
 90 95 100 105
 ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg 497
 Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val
 110 115 120
 att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat 545
 Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr
 125 130 135
 acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att 593
 Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile
 140 145 150
 ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa 641
 Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu
 155 160 165

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aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa      689
Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
170                               175                               180                               185
gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat      737
Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr
                               190                               195                               200
ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag      785
Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln
                               205                               210                               215
tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg      833
Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met
                               220                               225                               230
gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg      881
Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu
                               235                               240                               245
caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat      929
Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His
250                               255                               260                               265
caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat      977
Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn
                               270                               275                               280
aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct      1026
Asn Met Asp
gttttcatgga aggagatatt aaacatttgt ttaattttta tttaagtgtt atacctattt      1086
cagcaaataa aatattttcat tgcttgaaaa aaaaaaaaaa aaa      1129

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<211> 778

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 266..586

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<222> 266..307

<223> Von Heijne matrix

score 4.534746808071

seq ILVTVPGVCPAQC/CW

<400> 109

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taaattaatg cctcttttta aatactaact tgtactactt ttgtggctgt gaatggtatc      180
ttttattgaa ctgaggcagc ttttaaaaga cttgcctgat catttagagc actcccattg      240
agggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg      292
                               Met Ile Leu Val Thr Val Pro Gly Val
                               -10
tgt cca gca caa tgt tgc tgg gca gag cag agg ggc aga ggc tca ggt      340
Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly
-5                               1                               5                               10
atg tac ttc att gac aag tgg gca agg cca tcc tgg gta cca cat tgg      388
Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp
                               15                               20                               25
ctt aat gat ctc ttc att gtg aag tcc ggc tac ctc gtt tgc ata aga      436
Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg

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      30      35      40
act aca gta atc agg caa ggc att gtc aga att ggg agg aat aaa atc      484
Thr Thr Val Ile Arg Gln Gly Ile Val Arg Ile Gly Arg Asn Lys Ile
      45      50      55
agt gag tct gga agg agt gct ctg tat aca att gca aag aac aaa atg      532
Ser Glu Ser Gly Arg Ser Ala Leu Tyr Thr Ile Ala Lys Asn Lys Met
60      65      70      75
gtc atc ttt aag gta cct gat tgc atg cac tta aat gca gat tat ttt      580
Val Ile Phe Lys Val Pro Asp Cys Met His Leu Asn Ala Asp Tyr Phe
      80      85      90
gga gtt tgaaaaggga ctattaatga aatctttctt ttcctcctt tctctttttc      636
Gly Val
ccttccccgc cactgattca gtgagctgga gattggatca cagccgaagg agtaaagggtg      696
ctgcaatgat gttagctgtg gccactgtgg atttttcgca agaacattaa taaactaaaa      756
acttcaaaaa aaaaaaaaaa aa      778

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<222> 59..745

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<222> 59..160
<223> Von Heijne matrix
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      seq LGAAALALLLANT/DV

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atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
      -30      -25      -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Leu Ala Leu Leu Ala
      -15      -10      -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1      5      10
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15      20      25      30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
      35      40      45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
      50      55      60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
      65      70      75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
      80      85      90

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aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95                               100                               105                               110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
                               115                               120                               125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                               130                               135                               140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
                               145                               150                               155
ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac      682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
                               160                               165                               170
cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag act ttg      730
Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
175                               180                               185                               190
gcc tca gag aaa aaa tgattgtgtg aaactgccca gctcagggat aaccagggac      785
Ala Ser Glu Lys Lys
                               195
attcacctgt gttcatggga tgtattgttt ccactcgtgt ccctaaggag tgagaaaccc      845
atttatactc tactctcagt atggattatt aatgtatttt aatattctgt ttaggccac      905
taaggcaaaa tagcccaaaa acaagactga caaaaatctg aaaaactaat gaggattatt      965
aagctaaaaac ctgggaaata ggaggtttta aattgactgc caggctgggt gcagtggctc     1025
acacctgtaa tcccagcact ttgggaggcc aaggtgagca agtcacttga ggtcgggagt     1085
tcgagaccag cctgagcaac atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc     1145
cgggtgtggt ggcaggcacc tgtagtccca gctaccgggg aggctgaggc aggagaaatca     1205
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 <213> Homo sapiens

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 <222> 59..676

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 <222> 59..160
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 score 5.94384548075359
 seq LGAAALALLLANT/DV

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atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
                               -30                               -25                               -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
                               -15                               -10                               -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
1                               5                               10

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ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15                      20                      25                      30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
                      35                      40                      45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
                      50                      55                      60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
                      65                      70                      75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
                      80                      85                      90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
                      95                      100                      105                      110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
                      115                      120                      125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                      130                      135                      140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
                      145                      150                      155
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag      676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
                      160                      165                      170
taaacctact ttctgttctg gaagctgcta agatgatcaa accacagact ttggcctcag      736
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tcatgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaacccat ttatactcta      856
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tgagcaacat ggcgaaaacc cgtctctact aaaaatacaa aaatcacccg ggtgtgtgtg      1156
caggcacctg tagtccagc taccggggag gctgaggcag gagaatcact tgaacctggg      1216
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<211> 1617

<212> DNA

<213> Homo sapiens

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<222> 15..278

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<221> sig_peptide

<222> 15..146

<223> Von Heijne matrix

score 12.2610572403264

seq PLFLLLLLGSVTA/DI

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cctggggaat agtctggccc gctccttgga accacactca gactca atg gac tct 175
Met Asp Ser
-30
gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc 223
Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Arg Pro
-25 -20 -15
ttg ctt tca tcc tgt ggc ctc cca cca agc act gcc tca gct gtg cgc 271
Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
-10 -5 1
agg cta tgc tcc agg gga gtg tta aaa gga tca aat gaa aga agg gat 319
Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
5 10 15
atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tcg gac cga tac 367
Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
20 25 30 35
ctg gag agc cgc gat gcc tct cga ctg agt ggc cgg gac ccc tcc tca 415
Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp Pro Ser Ser
40 45 50
tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag 463
Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
55 60 65
ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag 511
Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
70 75 80
gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg 559
Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
85 90 95
aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag 607
Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
100 105 110 115
cag ggc aag ttc tgaaccagga gaggcagcct agacaaccaa gtggcagcag 659
Gln Gly Lys Phe
gtgggggcat tcttctagga atgaggggca tcagcccacc ccaggcacct cagtgggggtt 719
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tcacccact cgcctgtcca caggcttct tgtaagcaag tcagcagcac agctactcac 1559
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aaaaaaaaa aaaaa 1634

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<212> DNA
<213> Homo sapiens

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 <222> 223..417

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 <221> sig_peptide
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 seq LACVRESTSVAWA/CK

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 cctatccccg gccccgctcg ggcctttccc cttgcgcctt ggctcggtcg gctcgacgag 180
 cagtaagttc gtacccgccc tccgaagccg ggcgtgcatg gg atg gca gag ttg 234
 Met Ala Glu Leu
 -15
 gcg tgc gtg cgt gag tcc acc agt gtg gca tgg gca tgt aag gtg cgc 282
 Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala Cys Lys Val Arg
 -10 -5 1
 gga ggg act gca cct tct cca tca ggt gca gaa ggc cac gtc atg ctg 330
 Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly His Val Met Leu
 5 10 15 20
 aac aag agc cga gaa gta gaa tcg cca gtg tca agc cgt cca cgt tgt 378
 Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser Arg Pro Arg Cys
 25 30 35
 ggg atg ccc act gtt ccc cca gga tca ctc aag acc ctg tgacttgtgg 427
 Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr Leu
 40 45
 tcaactgatga gtggaccaag tgaagtccac aagatggctg ctgtggctcc aggcacacg 487
 tccacatgca aatccatcca gaggcaggaa ctgggaatag gcttggaggt ggccaggaca 547
 gcaagtgggc tgtctgtata aacctccccct ccacttgga aggaaaatca ccccccaagt 607
 cgattttctg tccatcttat tgatcagaga gcgttataaa ttcaccatt aaataatctg 667
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<210> 115
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 <222> 166..732

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 score 6.60662787180923
 seq KMVHLLVLSGAWG/MQ

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 gggcggtggga gtgaggtacc agattcagcc catttgccc cgacgcctct gttctcgga 120
 tccgggtgct gcggattgag gtcccgttc ctaacggact gcaag atg gag gaa ggc 177
 Met Glu Glu Gly

```

ggg aac cta gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca 225
Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser
-20 -15 -10 -5
ggg gcc tgg ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg 273
Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu
1 5 10
ctt ttc cga agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa 321
Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys
15 20 25
ctc ttc ccc ttc tac ttc cac atc tcc atg ggc tgt gsc ttc atc aac 369
Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Xaa Phe Ile Asn
30 35 40
ctc tgc atc ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg 417
Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp
45 50 55 60
gag gcc agc cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act 465
Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr
65 70 75
gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc 513
Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala
80 85 90
ctg caa acc gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc 561
Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly
95 100 105
agc cac cag ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc 609
Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro
110 115 120
aag tac agt gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc 657
Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser
125 130 135 140
tct ctt tgc aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct 705
Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
145 150 155
ggc ctt gcc ctg gaa ata agg agc ctc tagcatgggc cctgcatgct 752
Gly Leu Ala Leu Glu Ile Arg Ser Leu
160 165
aataaatgct tctccaaaaa aaaaaaaaaa aa 784

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<210> 116
 <211> 804
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..623

<220>
 <221> sig_peptide
 <222> 75..215
 <223> Von Heijne matrix
 score 8.34104221735598
 seq RLLLPCLVRMALC/AP

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agtacggtgg ccgacgggag tcagacgctg gggatgaatg aaggtgctgg gtgcaggatc 60
aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct 110
Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro

```

```

-45 -40
ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct 158
Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser
-35 -30 -25 -20
tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg 206
Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met
-15 -10 -5
gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag 254
Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys
1 5 10
aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att 302
Lys Leu Ile Leu Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile
15 20 25
gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc 350
Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser
30 35 40 45
aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag 398
Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu
50 55 60
tgc ggt ggc gtg atc tgc gct cac tgc aac ctc cac ctc ctg ggt tca 446
Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser
65 70 75
agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg 494
Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr
80 85 90
cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca 542
Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser
95 100 105
cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg 590
Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu
110 115 120 125
cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgccctggcct 643
Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala
130 135
atgtggtgga gtatttatta tacgtaggat gtgaatccct gaaatacaca ggcaaactaa 703
atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat 763
ttcaataaaaa gataattttt atacaaaaaa aaaaaaaaaa a 804

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<210> 117

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 30..335

<220>

<221> sig_peptide

<222> 30..71

<223> Von Heijne matrix

score 4.49063834776683

seq FLTALLWRGRIPG/RQ

<400> 117

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gcagagtctt gagcagcgcg gcaggcacc atg ttc ctg act gcg ctc ctc tgg 53
Met Phe Leu Thr Ala Leu Leu Trp
-10

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cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg ccg      101
Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg Pro
-5                      1                      5                      10
cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag      149
Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu
15                      20                      25
atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg      197
Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg
30                      35                      40
gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag      245
Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu
45                      50                      55
gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att      293
Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile
60                      65                      70
gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc      335
Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser
75                      80                      85
taatcctgag tcgtcaccct tggattttat ggatcacgga gctgaccatc tttacctggt      395
cctggaactg aaaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa      455
acaaacaaac acaaaaaaaaa aaaaaaaaaa      484

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<210> 118
 <211> 985
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21...752

<220>
 <221> sig_peptide
 <222> 21...107
 <223> Von Heijne matrix
 score 3.61056351168286
 seq FPLYLLNFLGLWS/WI

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<400> 118
gtttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc      53
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala
-25                      -20
att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg      101
Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu
-15                      -10                      -5
tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc      149
Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe
1                      5                      10
act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc      197
Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe
15                      20                      25                      30
agt aac ctg cag gag ttt gcg ggc ccc tcc ggg aaa ctc tcc ctg ctg      245
Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu
35                      40                      45
gaa gtg ggc tgt ggc acg ggg gcc aac ttc aag ttc tac cca cct ggg      293
Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly
50                      55                      60
tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg      341

```

Cys	Arg	Val	Thr	Cys	Ile	Asp	Pro	Asn	Pro	Asn	Phe	Glu	Lys	Phe	Leu	
		65					70					75				
atc	aag	agc	att	gca	gag	aac	cga	cac	ctg	cag	ttt	gag	cgc	ttt	gtg	389
Ile	Lys	Ser	Ile	Ala	Glu	Asn	Arg	His	Leu	Gln	Phe	Glu	Arg	Phe	Val	
	80					85					90					
gta	gct	gcc	ggg	gag	aac	atg	cac	cag	gtg	gct	gat	ggc	tct	gtg	gat	437
Val	Ala	Ala	Gly	Glu	Asn	Met	His	Gln	Val	Ala	Asp	Gly	Ser	Val	Asp	
95					100					105					110	
gtg	gtg	gtc	tgc	acc	ctg	gtg	ctg	tgc	tct	gtg	aag	aac	cag	gag	cgg	485
Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	Lys	Asn	Gln	Glu	Arg	
				115					120					125		
att	ctc	cgc	gag	gtg	tgc	aga	gtg	ctg	aga	ccg	gga	ggg	gct	ttc	tat	533
Ile	Leu	Arg	Glu	Val	Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr	
			130					135					140			
ttc	atg	gag	cat	gtg	gca	gct	gag	tgt	tcg	act	tgg	aat	tac	ttc	tgg	581
Phe	Met	Glu	His	Val	Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp	
		145					150					155				
caa	caa	gtc	ctg	gat	cct	gcc	tgg	cac	ctt	ctg	ttt	gat	ggg	tgc	aac	629
Gln	Gln	Val	Leu	Asp	Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn	
		160				165					170					
ctg	acc	aga	gag	agc	tgg	aag	gcc	ctg	gag	cgg	gcc	agc	ttc	tct	aag	677
Leu	Thr	Arg	Glu	Ser	Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys	
175					180					185					190	
ctg	aag	ctg	cag	cac	atc	cag	gcc	cca	ctg	tcc	tgg	gag	ttg	gtg	cgc	725
Leu	Lys	Leu	Gln	His	Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg	
				195				200						205		
cct	cat	atc	tat	gga	tat	gct	gtg	aaa	tagtgtgagc	tggcagttaa						772
Pro	His	Ile	Tyr	Gly	Tyr	Ala	Val	Lys								
			210				215									
gagctgaatg	gctcaaagaa	tttaaagctt	cagttttaca	tttaaaatgc	taggtgggtg											832
cctgtaatcc	caggtacttg	gaaggctgag	gcaggagaat	ctcttgaacc	cagaaggcga											892
aggttgagc	gaaccgagat	catgccattg	tactctagcc	tgggtgacaa	gagcaagact											952
ccgtctcaaa	aaaaaataaa	aaaaaaaaaa	aaa													985

<210> 119
 <211> 839
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 185..715

<220>
 <221> sig_peptide
 <222> 185..253
 <223> Von Heijne matrix
 score 9.49395175807817
 seq SLLFICFFGESFC/IC

<400> 119																
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cagctcctgg	tattttctgc	ttcccttcgt	agggaaattha	gttatatttat	tttattattt											120
agctaattta	gctattttta	aatagctaaa	ttttagctac	ttttttttca	attgacaaag											180
aagg atg tct	aat caa aga	cta ccg ctg	att ttt tct	ctg ttg ttt	atc											229
	Met Ser Asn	Gln Arg Leu	Pro Leu Ile	Phe Ser Leu	Leu Phe Ile											
		-20		-15												
tgc ttc ttc	ggg gag agt	ttc tgc att	tgt gat gga	act gtc tgg	aca											277


```

Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
-5 1 5
aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa gtt 325
Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val
10 15 20
aag ggt tct cca tct cac tgc ctg cct tat ctt ctg gat aaa cta tgc 373
Lys Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys
25 30 35 40
tgc gac ttt gct aac atg gat ata ttt cag ggt tgt tta tat ctc att 421
Cys Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile
45 50 55
tat aat tta tta caa gct gtc ttc ttc gtc tta ttt gtt ttg tct gtg 469
Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val
60 65 70
cat tac ctg tgg aag aaa tgg aag aaa cac caa aaa aag ctg aaa aag 517
His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys
75 80 85
caa gcc tcc tta gaa aaa cct ggt aat gat cta gaa agc cca ttg atc 565
Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile
90 95 100
aac aac att gac caa aca ctc cac aga gtg gca acc aca gca tca gtg 613
Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val
105 110 115 120
ata tac aag atc tgg gag cac agg tct cac cat cct tcc tct aag aaa 661
Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys
125 130 135
att aag cac tgc aaa tta aag aag aag agt aaa gaa gaa gga gcc aga 709
Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg
140 145 150
aga tac taaataaatg catatgcaaaa tgtagcttac tcaattatag atatcacaaa 765
Arg Tyr
agaaatctat catctaagga ttaaaaaattg ttctttggaa acctttataa aaaaaaaaga 825
aaaaaaaaa aaaa 839

<210> 120
<211> 583
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..527

<220>
<221> sig_peptide
<222> 54..116
<223> Von Heijne matrix
score 6.80928714315144
seq ALXSLNLAPPTVA/AP

<400> 120
aacgtcatct aggagcaccg agcagcttgg ctaaaagtaa ggggtgtcgtg ctg atg 56
Met
gcc ctg tgc gca ctg acc cgc gct ctg ccs tct ctg aac ctg gcg ccc 104
Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala Pro
-20 -15 -10 -5
ccg acc gtc gcc gcc cct gcc ccg agt ctg ttc ccc gcc gcc cag atg 152
Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met

```

				1				5				10				
atg	aac	aat	ggc	ctc	ctc	caa	cag	ccc	tct	gcc	ttg	atg	ttg	ctc	ccc	200
Met	Asn	Asn	Gly	Leu	Leu	Gln	Gln	Pro	Ser	Ala	Leu	Met	Leu	Leu	Pro	
				15				20				25				
tgc	cgc	cca	gtt	ctt	act	tct	gtg	gcc	ctt	aat	gcc	aac	ttt	gtg	tcc	248
Cys	Arg	Pro	Val	Leu	Thr	Ser	Val	Ala	Leu	Asn	Ala	Asn	Phe	Val	Ser	
				30				35				40				
tgg	aag	agt	cgt	acc	aag	tac	acc	att	aca	cca	gtg	aag	atg	agg	aag	296
Trp	Lys	Ser	Arg	Thr	Lys	Tyr	Thr	Ile	Thr	Pro	Val	Lys	Met	Arg	Lys	
				45				50				55				
tct	ggg	ggc	cga	gac	cac	aca	ggg	gct	gga	aac	gtg	cgt	aga	aca	gta	344
Ser	Gly	Gly	Arg	Asp	His	Thr	Gly	Ala	Gly	Asn	Val	Arg	Arg	Thr	Val	
				65				70				75				
ggc	cga	gta	tcc	aac	gtt	gat	cat	aac	aaa	cgg	gtc	att	ggc	aag	gca	392
Gly	Arg	Val	Ser	Asn	Val	Asp	His	Asn	Lys	Arg	Val	Ile	Gly	Lys	Ala	
				80				85				90				
ggg	cgc	aac	cgc	tgg	ctg	ggc	aag	agg	cct	aac	agt	ggg	cgg	tgg	cac	440
Gly	Arg	Asn	Arg	Trp	Leu	Gly	Lys	Arg	Pro	Asn	Ser	Gly	Arg	Trp	His	
				95				100				105				
cgc	aag	ggg	ggc	tgg	gct	ggc	cga	aag	att	cgg	cca	cta	ccc	ccc	atg	488
Arg	Lys	Gly	Gly	Trp	Ala	Gly	Arg	Lys	Ile	Arg	Pro	Leu	Pro	Pro	Met	
				110				115				120				
aag	agt	tac	gtg	aag	ctg	cct	tct	gct	tct	gcc	caa	agc	tgat	atc	cct	537
Lys	Ser	Tyr	Val	Lys	Leu	Pro	Ser	Ala	Ser	Ala	Gln	Ser				
				125				130				135				
gtactctaat aaaatgcccc cccccctca aaaaaaaaaa aaaaaa																583

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<210> 121
<211> 1024
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 129..686
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<220>
<221> sig_peptide
<222> 129..185
<223> Von Heijne matrix
      score 6.45239823575329
      seq  SVFLLMVNGQVES/AQ
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<400> 121
cttcgcgaag gtgtcgctgc caagaaacgt gtcctgcgcg ctacgccgtc tgtttctagg      60
gcaacgccgg cgtctcttag caaccgcgcg cggcctagggt ggggtccccc ggcacccccca      120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac      170
      Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn
              -15                      -10
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc      218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys
      -5              1              5              10
aag tac tgc ttt gtg tac gcc cag gac tgg gcc ccc aca gcg ggt ctg      266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu
              15              20              25
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa      314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln
      30              35              40

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[illegible]

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<210> 122
<211> 760
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 165..614
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<220>
<221> sig_peptide
<222> 165..305
<223> Von Heijne matrix
score 5.10820788278539
seq ALGLALCSTKALS/VG
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<400>	122
aatttccgat gccaggcacc ctcaaggcac agaggctggg gtcctatgttg ggggcacttg	60
gcctctccag gcctcgaaagg cttctcctgg gctgatgcga gctggggaac gggagggacg	120
gacgtgggag cgagaacgtc acactggagg cagctgggtg cacg atg ggg gac aga	176
Met Gly Asp Arg	
-45	
gtg aaa ggt agc aag tca aga gcc ttg gtg tca cca tgg cca cac acc	224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr	
-40 -35 -30	
ccg atg gct tcc ggc ttg agg gac ccg tgg ctg cag ccc aca gcc ctg	272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu	

```

-25          -20          -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct 320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro
-10          -5          1          5
ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc 368
Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala Ala Leu Ala Ala
10          15          20
ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc 416
Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr
25          30          35
agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg 464
Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg
40          45          50
ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct 512
Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro
55          60          65
gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg 560
Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp
70          75          80          85
cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat 608
Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His
90          95          100
ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc 664
Leu Cys
accaccatcc caccctgcc ctgccccact tccccagggt ctccttctg actcagtaaa 724
gatcaccgct gcctccctca aaaaaaaaaa aaaaaa 760

<210> 123
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..476

<220>
<221> sig_peptide
<222> 192..326
<223> Von Heijne matrix
score 6.60884760057354
seq FILLLLLSGPAEM/SA

<400> 123
actttttattg aaaaagacta cagcaaatca tactgaggtg aatgaagaca gtgaaatgaa 60
ggagaaggca ggctcctcttt atgttttcgc agctgggttca aggggttttg gggttttctat 120
ctagggttaaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac 180
acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt 230
Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu
-45          -40          -35
cta cac ctc cct cgc cct gac act tcc acc agg ttg ctc ctc acc tcc 278
Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser
-30          -25          -20
gtc tct gct ttt atc ctc tta ctg ctc ctt tca gga cca gca gaa atg 326
Val Ser Ala Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met
-15          -10          -5
tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct 374
Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala

```

```

1           5           10           15
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct 422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser
          20          25          30
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta 470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val
          35          40          45
aac ctt tgaaggtatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct 526
Asn Leu
          50
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa 586
aaaaaaaaa 594

<210> 124
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<212> DNA
<213> Homo sapiens

<220>
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<222> 16..297

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<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
      score 6.65836819891491
      seq FCGSACLLAVIRA/FF

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ttacacaggg gataa atg gca gca atc gag att gaa gtc aag cct aac cag 51
      Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln
          -25          -20          -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt 99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe
          -10          -5          1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg 147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu
          5          10          15
ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg 195
Gly Gly Met Gly Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp
          20          25          30
ctc ttt gcc tgg ttg ttt cca aga tgt act gtg cct ctt act ttc ggt 243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly
          35          40          45          50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc 291
Phe Glu Asn Met Arg Gly Leu Gly Val Ala Tyr Ala Cys Asn Pro
          55          60          65
agc act tagggaggcc gaggcgggag gatggcttga ggtccgtagt tgagaccagc 347
Ser Thr
ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaat tagccgggtg 407
tgggtggctcg tgccctgtggt cccagctgct ccggtggctg aggcgggagg atctcttgag 467
cttaggcttt tgagctatca tggcgccagt gcactccagc gtgggcaaca gagcgagacc 527
ctgtctctca aaaacaaaaa aaaaaaaaaa aa 559

<210> 125
<211> 744
<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> 216..635

<220>

<221> sig_peptide

<222> 216..335

<223> Von Heijne matrix

score 4.38054120608596

seq ITLVSAAPGKVIC/EM

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gctcgccctga ctcccgccct cttgcgctcc taggggcgga gaaggggtgcg ggctcttcgc 120
cctttgtgtc ctccctcttt cactaacttc tggactttcc agctcttccg aagttcgttc 180
ttgcgcaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag 233
Met Thr Ser Met Thr Gln
-40 -35
tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag 281
Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
-30 -25 -20
aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg 329
Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
-15 -10 -5
att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act 377
Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
1 5 10
ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg 425
Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
15 20 25 30
gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg 473
Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
35 40 45
aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att 521
Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
50 55 60
aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg 569
Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
65 70 75
gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac 617
Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
80 85 90
aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac 665
Thr Lys His Leu Gly Asn
95 100
ccaacaatga atatcaagta tagatttgac tcaaacaatt gtaatttttg aaataaacta 725
gcaaaaaaaaa aaaaaaaaaa 744

<210> 126

<211> 824

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 164..280

<220>
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 <222> 164..268
 <223> Von Heijne matrix
 score 5.73290676305402
 seq TLPLCPVTSPVWG/WS

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 ccaggagacc tacacagtgg cccacgagga gaatgtccgc tttgtgtccg aaggtagcga 120
 gcggggccag aggggtgcggc ataggctgct gggtcgcaaa acc atg gac ccg gga 175
 Met Asp Pro Gly
 -35
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe
 -30 -25 -20
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp
 -15 -10 -5 1
 agt cca ggg tgaccatcag gccctgggtg ggcgatgggg tgccctgggac 320
 Ser Pro Gly
 ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380
 ggtggcccg cccgtgaggg cgggccaagg cctgtgcagt acgtggagag gacccccaat 440
 ccccggtgc agaactttgt gccattttac cttagacgagt ggtgggcgca gcagttcctg 500
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560
 tgctgccagg agagaagcat ggccgctgc ccacccactg cgcctggctg ggtgccggcc 620
 acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggctgtccc 680
 aaccaagctg ccattggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc 740
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 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 68..301

<220>
 <221> sig_peptide
 <222> 68..190
 <223> Von Heijne matrix
 score 4.68908216483476
 seq AYLLYILLTGALQ/FG

<400> 127
 acatccggtg tggtcgacgg gtccctccaag agtttggggc gcggaccgga gtaccttgcg 60
 tgcagtt atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa 109
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu
 -40 -35 -30
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr
 -25 -20 -15
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu

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-10          -5          1          5
ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct 253
Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser
          10          15          20
tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga 301
Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
          25          30          35
taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac 361
tgctagctct gctttttatg caggagaaaa gccagaggt cactgtgtgt cagaacaact 421
ttctaacaaa catttattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc 481
caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa 526

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<210> 128
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 <212> DNA
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<220>
 <221> CDS
 <222> 179..427

<220>
 <221> sig_peptide
 <222> 179..298
 <223> Von Heijne matrix
 score 7.72883276007822
 seq CLVVVTMATLSLA/RP

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aatctaccca ggaacaaaac accagtgact gcagcagcag cggcagcgcc tcggttcctg 120
agccaccgcg aggtctgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag 178
atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt 226
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40          -35          -30          -25
acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc 274
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
          -20          -15          -10
acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag 322
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
          -5          1          5
gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag 370
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
          10          15          20
gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac 418
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
          25          30          35          40
aag agt aag taactgccc gctccgatgg tccccgagag aggagcatgg 467
Lys Ser Lys
agggaaagttc tgccgtgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccg 527
cggcccttgc ctttccccgc tgtgtctact ttcttgactt tcaaacctga gaataaacca 587
gtgttgctgc acataaaaaa aaaaaaaaaa a 618

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<210> 129
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 <212> DNA
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<220>
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 <222> 22..297

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 <222> 22..66
 <223> Von Heijne matrix
 score 4.68058603039206
 seq VLAGSLLGPTSRS/AA

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 Met Ala Val Leu Ala Gly Ser Leu Leu Gly
 -15 -10
 ccc acg agt agg tcg gca gcg ttg ctg ggt ggc agg tgg ctc cag ccc 99
 Pro Thr Ser Arg Ser Ala Ala Leu Leu Gly Gly Arg Trp Leu Gln Pro
 -5 1 5 10
 cgg gcc tgg ctg ggg ttc cca gac gcc tgg ggc ctc ccc acc ccg cag 147
 Arg Ala Trp Leu Gly Phe Pro Asp Ala Trp Gly Leu Pro Thr Pro Gln
 15 20 25
 cag gcc cgg ggc aag gct cgc ggg aat gag tat cag ccg agc aat atc 195
 Gln Ala Arg Gly Lys Ala Arg Gly Asn Glu Tyr Gln Pro Ser Asn Ile
 30 35 40
 aaa cgc aag aac aag cac ggc tgg gtc cgg cgc ctg agc acg ccg gcc 243
 Lys Arg Lys Asn Lys His Gly Trp Val Arg Arg Leu Ser Thr Pro Ala
 45 50 55
 ggc gtg cag gtc atc ctt cgc cga atg ctc aag ggc cgc aag tcg ctg 291
 Gly Val Gln Val Ile Leu Arg Arg Met Leu Lys Gly Arg Lys Ser Leu
 60 65 70 75
 agc cat tgaggatcgc gacgcagtcg gcggggaccc tcatggaagc atcgccctcg 347
 Ser His
 cctcggacct tgcctggcgc tatttttgca gggagctggg gagcaggaac gcctcggacc 407
 tgagtgtctt ccatattgtg ggtttgaagt ctggatggga gccttgccaa gtcccttttt 467
 aggtttttta attaggaagc atttcgaacc tgcgcaacag accaaagaac agtacaaaga 527
 acatccgtgt acccagtacc ctgactaccg actacctaca acccgtcctt gccccatcct 587
 gagttctttt gaagctgata tcaggcatcg gattatttct tctgtaaata ttccagaatg 647
 tatctctcca agatgagagc tcattaaaag ataattacaa agcttatcac atccaaaaga 707
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 aaaaaaaaa 776

<210> 130
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 9..845
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 <221> sig_peptide
 <222> 9..134
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 seq RSLALAAAPSSNG/SP

<400> 130

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ggt tgg cgg cgg ttc gag agg ctc tgg gcc ggc agt cta agc tct cgc	98
Gly Trp Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg	
-25 -20 -15	
agc ctg gct ctt gca gcc gca ccc tca agc aac gga tcc cca tgg cgc	146
Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg	
-10 -5 1	
ttg ttg ggc gcg ttg tgc ctg cag cgg cca cct gta gtc tcc aag ccg	194
Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Val Val Ser Lys Pro	
5 10 15 20	
ttg acc cca ttg cag gaa gag atg gcg tct cta ctg cag cag att gag	242
Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu	
25 30 35	
ata gag aga agc ctg tat tca gac cac gag ctt cgt gct ctg gat gaa	290
Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu	
40 45 50	
aac cag cga ctg gca aag aag aaa gct gac ctt cat gat gaa gaa gat	338
Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp	
55 60 65	
gaa cag gat ata ttg ctg gcg caa gat ttg gaa gat atg tgg gag cag	386
Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln	
70 75 80	
aaa ttt cta cag ttc aaa ctt gga gct cgc ata aca gaa gct gat gaa	434
Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu	
85 90 95 100	
aag aat gac cga aca tcc ctg aac agg aac cta gac agg aac ctt gtc	482
Lys Asn Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val	
105 110 115	
ctg tta gtc aga gag aag ttt gga gac cag gat gtt tgg ata ctg ccc	530
Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro	
120 125 130	
cag gca gag tgg cag cct ggg gag acc ctt cga gga aca gct gaa cga	578
Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg	
135 140 145	
acc ctg gcc aca ctc tca gaa aac aac atg gaa gcc aag ttc cta gga	626
Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly	
150 155 160	
aat gca ccc tgt ggg cac tac aca ttc aag ttc ccc cag gca atg cgg	674
Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg	
165 170 175 180	
aca gag agt aac ctc gga gcc aag gtg ttc ttc ttc aaa gca ctg cta	722
Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu Leu	
185 190 195	
tta act gga gac ttt tcc cag gct ggg aat aag ggc cat cat gtg tgg	770
Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp	
200 205 210	
gtc att aag gat gag ctg ggt gac tat ttg aaa cca aaa tac ctg gcc	818
Val Ile Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala	
215 220 225	
caa gtt agg agg ttt gtt tca gac ctc tgatgggccg agctgcctgt	865
Gln Val Arg Arg Phe Val Ser Asp Leu	
230 235	
ggacgggtgct cagacaagtc tgggattaga gcctcaagga cattgtgtga ttgcctcaca	925
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aaaaaaaaaaa aaa	998

<210> 131
 <211> 779
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..578

<220>
 <221> sig_peptide
 <222> 27..119
 <223> Von Heijne matrix
 score 4.50637135496675
 seq TALMVGAASLLEG/RP

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 Met Ala Cys Thr Thr Thr Ala Pro Ala
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 cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct 101
 Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
 -20 -15 -10
 gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga 149
 Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
 -5 1 5 10
 gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt 197
 Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
 15 20 25
 ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg 245
 Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
 30 35 40
 tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca 293
 Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
 45 50 55
 gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct 341
 Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
 60 65 70
 gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tcg 389
 Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
 75 80 85 90
 tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt 437
 Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
 95 100 105
 ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag 485
 Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
 110 115 120
 cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct 533
 Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
 125 130 135
 act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg 578
 Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
 140 145 150
 tgaacttctg tcttggttga gccatgggtt cattctcttt ttcagccatg tagcctgtgc 638
 tgtaactcag taccacatta gcaactagt aaagtcaatg tgggtaaatt tgtcattctt 698
 cagggttagaa catttcttcc ttttattctt gtgtttttgg ctaaataaac tgggaaatta 758
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<210> 132
 <211> 1025
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 408..710

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 <221> sig_peptide
 <222> 408..533
 <223> Von Heijne matrix
 score 5.66440183652506
 seq QLCFHLISWLYSWA/SQ

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 gacaaaaaca atagctacta caaacaatag gagtttataa ttatgtgctg atgtattcga 180
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 ggtggctctc accccaggga cctaggaaca gcctgtcacc acacaattac tttataaacc 300
 ctggagatga aaatctcctt gtcctcaaaa tacttccaga agaacaacca gatgggaagg 360
 accttgggtg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac 416
 Met Ala His
 -40
 gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga 464
 Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
 -35 -30 -25
 ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg 512
 Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
 -20 -15 -10
 agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt 560
 Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
 -5 1 5
 att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt 608
 Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
 10 15 20 25
 ctc att ggt cca gac gag gaa ggt atc cag cct caa gtc atc att gtg 656
 Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
 30 35 40
 gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac 704
 Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
 45 50 55
 aga gac tgagagttgg tgctggtggt tgtggtggca gatgatatta cctgaagaag 760
 Arg Asp
 ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt 820
 ccctggtgtc ttcattttcc tccgtctccc tgctgtccct taccctctgc ccaatctcat 880
 tactctggt cttgggagtt gccttctgag gatactccac tgggggtacc tgagcctgga 940
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 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 247..501

<220>
<221> sig_peptide
<222> 247..306
<223> Von Heijne matrix
score 6.43040298500966
seq LLLVTLVASTVPG/NS

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ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt 120
gggcttctga tgggtccctag aggtatcagc tactcagtca gaaaacatac atggggaaga 180
aactgaagtt catgccacaa actgtagcag ctttgggaaca gaagggacca gacaacctca 240
aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val
-20 -15 -10
gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336
Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala
-5 1 5 10
cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384
His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val
15 20 25
ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432
Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Val Gly Glu Pro Asn
30 35 40
gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480
Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn
45 50 55
tgt tct cac ggg cag gcc ttt tgaaccaccc tggtagagaa caccaaccct 531
Cys Ser His Gly Gln Ala Phe
60 65
ggtgcttttag gctgtctgtg ccatttctag gcaatgaacg agtagttact gtaccaaccc 591
aaaaaaaaaaaa aaaaaa 607

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agcagccctg caaaggtttt tccagcgctc ttgggaggtg ggctgtgccc tgccctggccc 180
acctggccca cctggcccac cattacctga agggaagcat gaacagcctt tgacgtggga 240
gtggcgactg ctgagaggga actgtctgta cacaagcaat gtagccttat gggacctgag 300

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tggagcccca acccacgcag ggcgtgktct tc atg gct ttt cct ggc caa tct 353
                                Met Ala Phe Pro Gly Gln Ser
                                -25
gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctg tca 401
Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser
-20 -15 -10
agt ctc tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa 449
Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu
-5 1 5 10
gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg 497
Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg
15 20 25
cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag 545
Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys
30 35 40
gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat 593
Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn
45 50 55
att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg 642
Ile Arg Gly
60
aatccagaat aactctgaag aagccgagta acaggcatga agtgaagaga aatcgctgta 702
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                                Met Ala Gln
cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca 166
Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr
-30 -25 -20 -15
gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct 214
Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro
-10 -5 1
ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg 262
Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu

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      5              10              15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg 310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Pro Ala Arg
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gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc 358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
      35              40              45              50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctgggggactt 406
Ile Pro Gly Gln Cys Pro
      55
ctcagcgcca gccattggc gcctgcgttg cccgcattcca ggccctgcgg caggccctgt 466
gctagcgtgt tcgcaccagg aacgcagggtg ctgggctgtc ggggaggcct caggccacct 526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa 586
atgaattact gttcaaaaaa aaaaa 611

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      seq RVLCAPAAGAVRA/LR

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                        -15              -10
ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt 99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5              1              5              10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa 147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
      15              20              25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac 195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
      30              35              40
cct cac cgc tgg tcg gtg ggc cat acc atg gga aag gga cat cag cgg 243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
      45              50              55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc 291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
      60              65              70              75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga 339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
      80              85              90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct 387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
      95              100              105
gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgctgggg 437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr

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110
ctggcaggaa gggagccgac agccgcccctt cggatttgat gtcacgtttg cccgtgactg 497
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tatgctgatt cgcgtgaagg cggagcagaa tctcagcaga tcggaaactg ctctcgcct 617
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cacttctggt gacacttgtc atccagtgtt agtttgcagg taatttgctt tctgagatag 797
aatatctggc agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc 857
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  Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
      -10 -5 1
tgg atc ggg aag cac cgg cgg ccg cgg ttc gtg tgc ttg cgc gcc aag 157
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
      5 10 15
cag aac atg atc cgc cgc ctg gag atc gat gcg gag aac cat tac tgg 205
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp
      20 25 30
ctg agc atg ccc tac atg acc cgg gag cag gag cgc ggc cac gcc gsg 253
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa
      35 40 45 50
dtg cgc agg agg gag gcc ttc gag gcc ata aag gcg gcc gcc act tcc 301
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
      55 60 65
aag ttc ccc ccg cat aga ttc att gcg gac cag ctc gac cat ctc aat 349
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
      70 75 80
gtc acc aag aaa tgg tcc taatcctgag tagtcaccct tggattttat 397
Val Thr Lys Lys Trp Ser
      85
ggatcacgga gctgaccatc tttacctggt cctggaactg aaaaactgta gcttgtgtga 457
aaatgagcct ttggaccagt ctttattaaa acaaacaac atgagtagtc tgcatatcga 517
atatctagag ctctaaaccc cccaatactt aaaagtctaa ttgctgtcct gtggtttcat 577
tagtctgata ggaagatagg gatttcctca gtcacagatg atattttgaa ggaaagctgc 637
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<222> 107., 178

score 6.19650168602189

<400> 138

157

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Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg	Glu	Gly	Glu	
205						210					215					
ctg	tgg	cac	atc	cga	gcc	cag	gca	ggc	cta	agc	gtg	gtg	gcc	atc	atg	883
Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val	Ala	Ile	Met	
220					225					230					235	
gcc	gtc	gac	atc	ttc	ttt	cac	ttc	ttc	tac	atc	ctc	act	atc	ccc	agc	931
Ala	Val	Asp	Ile	Phe	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr	Ile	Pro	Ser	
			240						245					250		
gac	ctc	aag	ttc	gcc	aac	cgc	ctc	cca	gac	att	gcc	ctc	gct	ggc	cta	979
Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu	Ala	Gly	Leu	
255							260						265			
gcc	tat	tca	aac	ctg	gtg	tat	gac	tgg	gtg	aag	gcg	gcc	gtc	ctc	ttt	1027
Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala	Val	Leu	Phe	
270						275					280					
ggg	gtt	gtc	aac	act	gtg	gca	tgc	ctc	gac	cac	ctg	gac	cca	ccc	cag	1075
Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp	Pro	Pro	Gln	
285					290						295					
cct	ccc	aag	tgc	atc	acc	gca	ctc	tac	gtc	ttt	gcg	gaa	acg	cac	ttt	1123
Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu	Thr	His	Phe	
300					305					310					315	
gac	cgt	ggc	atc	aac	gac	tgg	ctt	tgc	aaa	tat	gtg	tat	aac	cac	att	1171
Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr	Asn	His	Ile	
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Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala	Thr	Val	Ala	
			335					340					345			
aca	ttt	gcc	atc	acc	aca	ctg	tgg	ctt	ggg	cct	tgt	gac	att	gtc	tac	1267
Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp	Ile	Val	Tyr	
350						355					360					
ctg	tgg	tca	ttc	ctt	aac	tgc	ttt	ggc	ctc	aac	ttt	gag	ctc	tgg	atg	1315
Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu	Leu	Trp	Met	
365					370						375					
caa	aaa	ctg	gca	gag	tgg	ggg	ccc	cta	gca	cga	att	gag	gcc	tct	ctg	1363
Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu	Ala	Ser	Leu	
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Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly	Ala	Met	Asn	
				400					405					410		
ttc	tgg	gcc	atc	atc	atg	tac	aac	ctt	gtg	agc	ctg	aac	agc	ctc	aaa	1459
Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn	Ser	Leu	Lys	
			415					420					425			
ttc	aca	gag	ctg	gtt	gcc	cgg	cgc	ctg	cta	ctc	aca	ggg	ttc	ccc	cag	1507
Phe	Thr	Glu	Leu	Val	Ala	Arg	Arg	Leu	Leu	Leu	Thr	Gly	Phe	Pro	Gln	
430						435						440				
acc	acg	ctg	tcc	atc	ctg	ttt	gtc	acc	tac	tgt	ggc	gtc	cag	ctg	gta	1555
Thr	Thr	Leu	Ser	Ile	Leu	Phe	Val	Thr	Tyr	Cys	Gly	Val	Gln	Leu	Val	
445					450						455					
aag	gag	cgt	gag	cga	acc	ttg	gca	ctg	gag	gag	gag	cag	aag	cag	gac	1603
Lys	Glu	Arg	Glu	Arg	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Lys	Gln	Asp	
460					465				470						475	
aaa	gag	aag	ccg	gag	taggagggag	cgggtagagg	gatgggctct	gctcagctat								1658
Lys	Glu	Lys	Pro	Glu												
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tcttgggccca	gatggggcct	gaccgataga	ataaaagact	tttctacaac	aaaaaaaaaa											1718
aaaaaaa																1725

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 1.0 × 10⁸ cells/ml. The cells were then mixed with the plant tissue and the transformation efficiency was determined. The results are shown as the mean ± SD of three independent experiments. The transformation efficiency was significantly different from the control (p < 0.05) by the Student's *t*-test.

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seq FCVCVIAIGVVOA/LI
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159

[illegible]

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ttgtacacgg	tagttattga	gttgagtaac	atagtttggt	ctgagtcatt	tgttccacat		180	
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160

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seq LGLCSLLVGEAEA/PS

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Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
-20 -15 -10
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg 154
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
-5 1 5
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Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
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acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt 250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
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Val Tyr Lys Pro Ile Arg Arg Arg
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gcttctcagt gtttctgact gtacttggtt aaagtaagac ctgaaagctc caaaggtcag 544
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ccaaaaagat tcaaaagagc aagtggaatc tctaaga atg gct tcc agc cac tgg      175
                               Met Ala Ser Ser His Trp
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aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa      223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln
-40                               -35                               -30
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Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile
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ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc      319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe
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Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val
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Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn
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Ile Arg Lys Arg Glu Thr Glu Val Val
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Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val
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caa ctg cag ggt ggg aga ttc ctg atg gga aca aat tct cca gac agc      145
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
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aga gat ggt gaa ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc      193
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
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Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
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ttt gag gac ttt gtc tct gat gag ctg aga aac aaa gcc acc cag cca      337
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
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Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Thr Ala
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cca acc tgt ggc agg gaa agt tcc cca agg gag aca aag ctg agg atg      433
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met
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Ala Ser Met Glu Ser Pro Gln
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<210> 144
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 <213> Homo sapiens

<220>
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cctggactgg tcatatacct cttgtggccc tggcagaatc aagatgaggc cctgtcatgc      180
ctccccagtg aggcctacag tctgagcaga cagcatggcc tgccactggc agtgaacacc      240
atg tct gca gga ggt ggc cgg gcc ttt gct tgg caa gtg ttc ccc ccc      288
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
  1              5              10              15

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Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro	
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Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala	
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gta	gag	gcc	ttc	ctg	atg	gat	gag	ggc	cgc	tgg	gag	cgt	cgg	gcc	acc	576
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr	
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Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met	
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gaa	gcc	ttt	gat	ctg	gag	gcc	cgt	aca	tgg	acc	cgg	cat	cca	agc	cta	864
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu	
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Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly	
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Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	
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Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys	
		305			310				315						320	
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Arg Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg
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ggc gtc agt ttc aaa ctg gaa gaa aaa acc gcc cac agc agc ctg gca 146
Gly Val Ser Phe Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala
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Pro Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val
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Val Leu Ala Asp Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val
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Thr Val Lys Arg Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp
95 100 105
atg tcc cgg gat agc tgc att ggt gtt gat gat cgt tcc tgg gtg ttc 386
Met Ser Arg Asp Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe
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Thr Tyr Ala Gln Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala
125 130 135 140
cca gtt gag ggt att ggg cag cca gag aag gtg ggg ctg ttg ctg gag 482
Pro Val Glu Gly Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu

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Ile	Gly	Glu	Leu	Ala	Pro	Gly	Ser	Phe	Leu	Ala	Ala	Val	Val	Asp	Ala					
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Cys Pro Leu Leu Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly																	
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Phe Ile Ser Ala Gln Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro																	
30 35 40																	
gaa gat tta caa ctg aag aat gca aga tta tta tgt att tgg cag ctg																	197
Glu Asp Leu Gln Leu Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu																	
45 50 55																	
aga aca ata ctt agt gga tac cat cga ata gta caa cag aga atg cag																	245
Arg Thr Ile Leu Ser Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln																	

60		65		70		75	
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His Ser Pro Asp Leu Met Ser Phe Met Met Glu Leu Lys Met Leu Leu							
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Glu Val Ala Leu Lys Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro							
ccc cag ttc tac tca agc ctt att gaa gag ata gga act ctt ggt tgg							389
Pro Gln Phe Tyr Ser Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp							
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Asp Lys Leu Val Tyr Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys							
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Ala Glu Asp Ala Ser Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys							
gca aag tat cct gca gaa tca cca gat tat ttt gtg gat ttt cct gtt							533
Ala Lys Tyr Pro Ala Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val							
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Pro Phe Cys Ala Ser Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr							
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Ser Gln Phe Leu Ala Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val							
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Met Asp Glu Ile Asp Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro							
cca cgg agt gca aca gca cgc aga att gca tta ggt aat aat gtt tcc							725
Pro Arg Ser Ala Thr Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser							
ata aat ata gag gta gac ccc agg cat cct act atg ctt cct gag tgc							773
Ile Asn Ile Glu Val Asp Pro Arg His Thr Met Leu Pro Glu Cys							
ttc ttt ctt gga gct gac cat gtg gta aaa ccc ctg gga att aag ctg							821
Phe Phe Leu Gly Ala Asp His Val Val Lys Pro Leu Gly Ile Lys Leu							
agc agg aac ata cat ttg tgg gat cca gaa aat agt gtg tta caa aat							869
Ser Arg Asn Ile His Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn							
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Leu Lys Asp Val Leu Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu							
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Lys Ser Asp Phe Thr Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu							
gac ggt acc att cct gat caa gtg tgt gat aat tcc cag tgt gga caa							1013
Asp Gly Thr Ile Pro Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln							
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Pro Phe His Gln Ile Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr							
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Ser Arg Gln Ser Phe Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser							
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<221> CDS

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ggt gac cga gtt act cca gct gtt gtt gct tac tca gaa aat gaa gag 207

35 40 45

Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn

aca gta atg aaa gta aag cag atc ctg ggc aga agc tcc agt gat cca 303

65 70 75

Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys

aat ggg aaa tta cga tat gaa ata gat act gga gaa gaa aca aaa ttt 399

95	100	105	110
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Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu

acg gca cat tct gta ttg ggc tca gat gca aat gat gta gtt att act 495

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gct aga gct gct gga ttt aat gtt ttg cga tta att cac gaa ccg tct 591

160 165 170

Ala Ala Leu Leu Ala Tyr Gly Ile Gly Gln Asp Ser Pro Thr Gly Lys

agg aat att ttg gtg ttt aag ctt gga gga aca tcc tta tct ctc agc 687

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Val	Met	Glu	Val	Asn	Ser	Gly	Ile	Tyr	Arg	Val	Leu	Ser	Thr	Asn	Thr		
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gat	gat	aac	atc	ggg	ggg	gca	cat	ttc	aca	gaa	acc	tta	gca	cag	tat		783
Asp	Asp	Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr		
		225					230					235					
cta	gct	tct	gag	ttc	caa	aga	tcc	ttc	aaa	cat	gat	gtg	aga	gga	aat		831
Leu	Ala	Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn		
	240					245					250						
gcg	cga	gcc	atg	atg	aaa	tta	acg	aac	agt	gct	gaa	gta	gcg	aaa	cat		879
Ala	Arg	Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His		
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tct	ttg	tca	acc	ttg	gga	agt	gcc	aac	tgt	ttt	ctt	gac	tca	tta	tat		927
Ser	Leu	Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr		
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gaa	ggg	caa	gat	ttt	gat	tgc	aat	gtg	tcc	aga	gca	aga	ttt	gaa	ctt		975
Glu	Gly	Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu		
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Leu	Cys	Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu		
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Leu	Asp	Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu		
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tgt	gga	ggg	tct	tct	cga	atc	cca	aag	cta	cag	caa	ctg	att	aaa	gat		1119
Cys	Gly	Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp		
335					340					345					350		
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Leu	Phe	Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val		
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atc	cct	att	ggg	gca	gct	ata	gaa	gca	gga	att	ctt	att	ggg	aaa	gaa		1215
Ile	Pro	Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu		
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aac	ctg	ttg	gtg	gaa	gac	tct	ctt	atg	ata	gag	tgt	tca	gcc	aga	gat		1263
Asn	Leu	Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp		
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Ile	Leu	Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val		
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ctg	ttt	cca	tca	ggg	act	cct	ttg	cca	gct	cga	aga	caa	cac	aca	ttg		1359
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415					420					425					430		
caa	gcc	cct	gga	agc	ata	tct	tca	gtg	tgc	ctt	gaa	ctc	tat	gag	tct		1407
Gln	Ala	Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser		
				435					440					445			
gat	ggg	aag	aac	tct	gcc	aaa	gag	gaa	acc	aag	ttt	gca	cag	gtt	gta		1455
Asp	Gly	Lys	Asn	Ser	Ala	Lys	Glu	Glu	Thr	Lys	Phe	Ala	Gln	Val	Val		
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ctc	cag	gat	tta	gat	aaa	aaa	gaa	aat	gga	tta	cgt	gat	ata	tta	gct		1503
Leu	Gln	Asp	Leu	Asp	Lys	Lys	Glu	Asn	Gly	Leu	Arg	Asp	Ile	Leu	Ala		
		465					470					475					
gtt	ctt	act	atg	aaa	agg	gat	gga	tct	tta	cat	gtg	aca	tgc	aca	gat		1551
Val	Leu	Thr	Met	Lys	Arg	Asp	Gly	Ser	Leu	His	Val	Thr	Cys	Thr	Asp		
	480					485					490						
caa	gaa	act	gga	aaa	tgt	gaa	gca	atc	tct	att	gag	ata	gca	tct			1596
Gln	Glu	Thr	Gly	Lys	Cys	Glu	Ala	Ile	Ser	Ile	Glu	Ile	Ala	Ser			

495 500 505
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gtgggacc atg tac aac act gga aga cac gta tcc ctt cgc ctg gac aag 170
Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys
1 5 10
gag cac ttg gtc aac ata tct gga ggg ccc atg aca tac agc cac cgg 218
Glu His Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg
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ctg gag gag atc cga cta cac ttt ggg agt gag gac agc caa ggg tcg 266
Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser
35 40 45
gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg 314
Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg
50 55 60
gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca 362
Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
65 70 75
tagaaaaagt ctgctgaccc ctgaattaca gtatgagcca ttcggaatgc atttctcttt 422
aaaagttctc gcctcattca gtgtctggaa cacagtgggt gctccccaat aggtgacacc 482
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Met Ala Thr
1
cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg gtg 165
His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met Val
5 10 15
ggc aca gtg gct gtc act gtc atg cct cag tgg ata gtg tcg gcc ttc 213
Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe
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Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu Trp	
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atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc tat	309
Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr	
55 60 65	
gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga ctg	357
Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu	
70 75 80	
atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc atc	405
Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala Ile	
85 90 95	
ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg aag	453
Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val Lys	
100 105 110 115	
gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc atg	501
Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met	
120 125 130	
gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga gat	549
Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp	
135 140 145	
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Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
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cagtatgtgt agttgtgtat gtttttttaa ctttactata aagccatgca aatgacaaaa	834
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gacatttcac	aatcca	aaa ttgccgtgg atg aac tct	tta ctt cac ttc ggg Met Asn Ser Leu Leu His Phe Gly	173
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	10 15 20			
cct gga aat cat acc cac cag gca tct tat aag cca	ttg ttg aag caa	269		
Pro Gly Asn His Thr His Gln Ala Ser Tyr Lys Pro Leu Leu Lys Gln				
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Val Val Glu Glu Ile Phe His Pro Glu Arg Pro Asp Ser Val Asp Ile				
	45 50 55			
gaa cac atg tct tca gcc ctc act gat ctc ctt aaa act gga ttt agc	365			
Glu His Met Ser Ser Gly Leu Thr Asp Leu Leu Lys Thr Gly Phe Ser				
	60 65 70			
atg ttc atg aag gtg agc cgg cct cat cct agt gac tac ccc ctc ctg	413			
Met Phe Met Lys Val Ser Arg Pro His Pro Ser Asp Tyr Pro Leu Leu				
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Ile Leu Phe Val Val Gly Gly Val Thr Val Ser Glu Val Lys Met Val				
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Lys Asp Leu Val Ala Ser Leu Lys Pro Gly Thr Gln Val Ile Val Leu				
	105 110 115 120			
tcc aca cga ctc ctg aag cca ctt aac att cct gag ctg tta ttt gca	557			
Ser Thr Arg Leu Leu Lys Pro Leu Asn Ile Pro Glu Leu Leu Phe Ala				
	125 130 135			
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Thr Asp Arg Leu His Pro Asp Leu Gly Phe				
	140 145			
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Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	Arg	Met	Gln	Cys	Lys	Ile		
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Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	Asp	Leu	Gln	Ala	Ala	Arg	Gly		
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Leu	Met	Cys	Ala	Ala	Ser	Val	Met	Ser	Phe	Leu	Ala	Phe	Met	Met	Ala		
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Ile	Leu	Gly	Met	Lys	Cys	Thr	Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val		
	100					105					110						
aag	gct	cac	att	ctg	ctg	acg	gct	gga	atc	atc	ttc	atc	atc	gcg	ggc	562	
Lys	Ala	His	Ile	Leu	Leu	Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Ala	Gly		
	115				120					125					130		
atg	gtg	gtg	ctc	atc	cct	gtg	agc	tgg	gtt	gcc	aat	gcc	atc	atc	aga	610	
Met	Val	Val	Leu	Ile	Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg		
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Glu	Ala	Leu	Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly		
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gga	gct	ctg	ttc	tgc	tgc	gtt	ttt	tgt	tgc	aac	gaa	aag	agc	agt	agc	754	
Gly	Ala	Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser		
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Tyr	Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His		
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Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val			
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 Met Arg Leu Gln Asp
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 cgc atc gcc acg ttc ttc ttc cca aaa ggc atg atg ctc acc acg gct 162
 Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala
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 Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val
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 His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr
 40 45 50
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 Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala
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 Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
 70 75 80 85
 cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg 402
 His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
 90 95 100
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 Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
 10 15 20
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 Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
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 gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc 196

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Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro	
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Ser	Leu	Gln	His	Ala	Arg	Val	Leu	Gln	Tyr	Arg	Glu	Leu	Leu	Asp	Ala	
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His	Leu	Ala	Asn	Ala	Thr	Thr	Asp	Leu	Met	Lys	Leu	Asp	His	Glu	Glu	
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Arg	Lys	Leu	Glu	Asn	Glu	Gly	Gln	Lys	Cys	Glu	Leu	Trp	Leu	Cys	Gly	
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Cys	Ala	Phe	Thr	Leu	Ala	Asp	Val	Leu	Leu	Gly	Ala	Thr	Leu	His	Arg	
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Tyr	Leu	Ile	Gly	Ile	Ala	Ala	Ile	Val	Val	Ala	Val	Ile	Met	Ile	Phe
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Val	Tyr														
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Lys	Gln	Asn	Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly		
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Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu	Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg		
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Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu	Val	Pro	Val	Met	Leu	Thr	Glu	Gln		
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Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr	Val	Pro	Glu	Leu	Gly	Thr	Glu	Gly		
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Gln	Glu	Leu	Asp	Ser	Arg	Pro	Gln	Leu	Arg	Ser	Val	Leu	Leu	Cys	Gly		
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Ile	Glu	Ala	Gln	Ala	Cys	Ile	Leu	Asn	Thr	Thr	Leu	Asp	Leu	Leu	Asp		
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Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala
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Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala
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gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc      698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala
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Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu
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His
205
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tcggcccccg gccacttcac ggggcgggaa ggggagggga agaagagtct cagactgtgg      1039
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Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile
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Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys
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aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt      259
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu
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gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta      307
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val
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ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta      355
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
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gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag      403
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu
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ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt      451
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly
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ctg gcc ttt gcg tcc ttc tac ctg gca ggg aag tta cac tgc ttc aca	499
Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr	
120 125 130	
cca caa ggc cgt ggg aaa tct tgg agg ttc tgt gcc ttt ctg tca cct	547
Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro	
135 140 145 150	
cta ctt ttt gca gct gtg att gca ctg tcc cgc aca tgt gac tac aag	595
Leu Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys	
155 160 165	
cat cac tgg caa gat ctg ctc aaa tgc acc aac act gcc aag	637
His His Trp Gln Asp Leu Leu Lys Cys Thr Asn Thr Ala Lys	
170 175 180	
tgactaaggt agaaaagaaa aatgacaggt atcgatcatct gaaggacaga tgaatctttt	697
tctgcccctt cttcacaatg gaataaagg aacaattatg ggatgtcatc agaatggatg	757
ccataggacc tacagctccc tttctcttta ttgtgattat actttaata tgacattgtc	817
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atctgcttag ttctacaaag tggagtttct gggcatcatt cttcatttct gtacacaaag	180
tgctgtgaag ctcaagaaga aatagctctg cacaggaacg atg tgc act gcc cta	235
Met Cys Thr Ala Leu	
1 5	
ctg ctt ctt tat cta aga tgg tgt ttc aac tta aaa ctt gtg aat gtg	283
Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu Lys Leu Val Asn Val	
10 15 20	
aaa tat gag cca aaa gac tct ctc ggc cct gaa atg acc ttt gta gca	331
Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu Met Thr Phe Val Ala	
25 30 35	
gat gct gcc aga ggc ccc ctg tta tcc tcc ctg gac tct cca gct aac	379
Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu Asp Ser Pro Ala Asn	
40 45 50	
ctg atg tca act gcc agt gtg tgc atc tcc tta cct gag ggc tgt tct	427
Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu Pro Glu Gly Cys Ser	
55 60 65	
ggg ggc agg agt cct tgc tac tca cag aaa tgg cca cca gaa gtg cca	475
Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp Pro Pro Glu Val Pro	
70 75 80 85	
gaa aaa tta acc tcc ctt ggc cag cag tcc tca acc agc tcc ctc act	523
Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser Thr Ser Ser Leu Thr	
90 95 100	
gac act gat gtg cag gtg tct cct atg ctg gtt gct gga gtc aac cac	571
Asp Thr Asp Val Gln Val Ser Pro Met Leu Val Ala Gly Val Asn His	
105 110 115	
agc agc agc ctt ctt gac aac ata ccc ttc act ggc tgc ctt cct ttc	619
Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr Gly Cys Leu Pro Phe	
120 125 130	

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cat ctc tct tct tca ctc ccc tac cta tgt ctc cta ggc tct ccc ttc      667
His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu Leu Gly Ser Pro Phe
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Lys
150

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atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg      176
                               Met Glu Asp Pro
                               1
aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt      224
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
5              10              15              20
ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc      272
Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys
              25              30              35
acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac      320
Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His
              40              45              50
atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg      368
Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly
              55              60              65
gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa      416
Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys
              70              75              80
gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc      464
Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr
85              90              95              100
ctg ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac      512
Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp
              105              110              115
tgt ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag      560
Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln
              120              125              130
atg cat gag gtc cgt gcc cct cct gcc acc ttc gcc tgc aca gag tgc      608
Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys
              135              140              145
ggg cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg      656
Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg
              150              155              160
cat gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac      704
His Ala Arg Gly Glu Leu
165              170
gggtggctct gtggctggta ggactcacc atgatatggg gtgcaggaac tctggggggc      764
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agattctcaa aaaaaaaaaa aaaaaa      849

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 atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg 176
 Met Glu Asp Pro
 1
 aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224
 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
 5 10 15 20
 ccc cag ccc agg agg caa cat ctg cca cct ggg ggc ccc gaa gtg cac 272
 Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly Pro Glu Val His
 25 30 35
 ccg ctg cct cat cac ctt cgc aga ttc caa gtt cca gga gcg tca cat 320
 Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro Gly Ala Ser His
 40 45 50
 gaa gcg gga gca ccc agc gga ctt cgt ggc cca gaa gct gca ggg ggt 368
 Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu Ala Ala Gly Gly
 55 60 65
 cct ctt cat ctg ctt cac ctg cgc ccg ctc ctt ccc ctc ctc caa agc 416
 Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro Leu Leu Gln Ser
 70 75 80
 cct aat cac cca cca gcg cag cac ggt cca gcc gcc aag ccc acc ctg 464
 Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu
 85 90 95 100
 ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac tgt 512
 Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
 105 110 115
 ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag atg 560
 Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln Met
 120 125 130
 cat gag gtc cgt gcc cct cct ggc acc ttc gcc tgc aca gag tgc ggt 608
 His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys Gly
 135 140 145
 cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg cat 656
 Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg His
 150 155 160
 gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac ggggtggctct 711
 Ala Arg Gly Glu Leu
 165
 gtggctggta ggactcacc atgatatggg gtgcaggaac tctggggggc ctgaaggatt 771
 tgcttccctc ccctgggaag gcagagggct cttaataaag aggaccaga agattctcaa 831
 aaaaaaaaaa aaaaa 846

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                        Met Ala Thr Pro Asn Asn Leu Thr Pro
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acc aac tgc agc tgg tgg ccc atc tcc gcg ctg gag agc gat gcg gcc      102
Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala Ala
10                               15                               20                               25
aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc cat      150
Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala His
                               30                               35                               40
tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc agc      198
Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser
                               45                               50                               55
tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg tgc gag      246
Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu
                               60                               65                               70
gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc tgg ttc      294
Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe
                               75                               80                               85
atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac cgc gac      342
Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp
90                               95                               100                               105
aac atc atc agt gac tat gac cag atc att gac tat gtg gag cgc acc      390
Asn Ile Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu Arg Thr
                               110                               115                               120
ttc aca gga gag cac gtg gtg gcc ctg atg ccc gag gtg ggc agc ctg      438
Phe Thr Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly Ser Leu
                               125                               130                               135
cag cac gca cgg gtg ctg cag tac cgg gag ctg ctg gac gca ctg ccc      486
Gln His Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala Leu Pro
                               140                               145                               150
atg gat gcc tac acg cat ggc tgc atc ctg cat ctc gag ctc acc acc      534
Met Asp Ala Tyr Thr His Gly Cys Ile Leu His Leu Glu Leu Thr Thr
                               155                               160                               165
gac tcc atg atc ccc aag tac gcc acg gcc gag atc cgc aga cat tta      582
Asp Ser Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg His Leu
170                               175                               180                               185
gcc aat gcc acc acg gac ctc atg aaa ctg gac cat gaa gag gag ccc      630
Ala Asn Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu Glu Pro
                               190                               195                               200
cag ctc tcc gag ccc tac ctt tct aaa caa aag aag ctc atg gcc aag      678
Gln Leu Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met Ala Lys
                               205                               210                               215
atc ttg gag cat gat gat gtg agc tac ctg aag aag atc ctc ggg gaa      726
Ile Leu Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu
                               220                               225                               230
ctg gcc atg gtg ctg gac cag att gag gcg gag ctg gag aag agg aag      774
Leu Ala Met Val Leu Asp Gln Ile Glu Ala Glu Leu Glu Lys Arg Lys
                               235                               240                               245
ctg gag aac gag ggg cag aaa tgc gag ctg tgg ctc tgt ggc tgt gcc      822
Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Ala
250                               255                               260                               265
ttc acc ctc gct gat gtc ctc ctg gga gcc acc ctg cac cgc ctc aag      870
Phe Thr Leu Ala Asp Val Leu Leu Gly Ala Thr Leu His Arg Leu Lys

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270	275	280	
ttc ctg gga ctg tcc aag aaa tac tgg gaa gat ggc agc cgg ccc aac			918
Phe Leu Gly Leu Ser Lys Lys Tyr Trp Glu Asp Gly Ser Arg Pro Asn			
285	290	295	
ctg cag tcc ttc ttt gag agg gtc cag aga cgc ttt gcc ttc cgg aaa			966
Leu Gln Ser Phe Phe Glu Arg Val Gln Arg Arg Phe Ala Phe Arg Lys			
300	305	310	
gtc ctg ggt gac atc cac acc acc ctg ctg tgc gcc gtc atc ccc aat			1014
Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn			
315	320	325	
gct ttc cgg ctg gtc aag agg aaa ccc cca tcc ttc ttc ggg gcg tcc			1062
Ala Phe Arg Leu Val Lys Arg Lys Pro Pro Ser Phe Phe Gly Ala Ser			
330	335	340	345
ttc ctc atg ggc tcc ctg ggt ggg atg ggc tac ttt gcc tac tgg tac			1110
Phe Leu Met Gly Ser Leu Gly Gly Met Gly Tyr Phe Ala Tyr Trp Tyr			
350	355	360	
ctc aag aaa aaa tac atc tagggccagg cctggggcctt ggtgtctgac			1158
Leu Lys Lys Lys Tyr Ile			
365			
aaaaaamaaa aaaaaaaa			1176
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gcaccttccg gaaa atg gcg gct gcc agg ccc agc ctg ggc cga gtc ctc			170
Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu			
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cca gga tcc tct cct gtt cct gtg tgacatgcag gagaagttcc gccacaacat			224
Pro Gly Ser Ser Pro Val Pro Val			
15	20		
cgctacttc ccacagatcg tctcagtggc tgcccgcgatg ctcaagggtgg ccggtctgct			284
tgagggtgcca gtcagtctga cggagcagta cccacaaggc ctgggcccga cgggtgccga			344
gctggggact gagggccttc ggccgctggc caagacctgc ttcagcatgg tgccctgcct			404
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acaggcctgc atcttgaaca cgacctgga cctcctagac cgggggctgc aggtccatgt			524
ggtggtggac gectgctcct cagcagccca ggtggaccgg ctggtggctc tggcccgcct			584
gagacagagt ggtgccttcc tctccaccag cgaagggtc attctgcagc ttgtgggcga			644
tgccgtccac cccagttca aggagatcca gaaactcacc aaggagcccg cccagacag			704
cggactgctg ggccctcttc aaggccagaa ctccctcctc cactgaactc caacctgcc			764
ttgagggaag accacctctc tgtcaccggg acctcagtgg aagcccgctc ccccatccc			824
tgatcccaa gagggtgctg atccaccagg agtgccggcc ccttggggggg ggcagggtgc			884
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gcagaagtag cagttccgga gtccagctgg ctaaaactca tcccagagga ta atg gca      178
                                   Met Ala
                                   1
acc cat gcc tta gaa atc gct ggg ctg ttt ctt ggt ggt gtt gga atg      226
Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
                                   5      10      15
gtg ggc aca gtg gct gtc act gtc atg cct cag tgg aga gtg tcg gcc      274
Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
                                   20      25      30
ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu
                                   35      40      45      50
tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc      370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile
                                   55      60      65
tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga      418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly
                                   70      75      80
ctg atg tgt gct gct tcc gtg atg tcc ttc ttg gct ttc atg atg gcc      466
Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala
                                   85      90      95
atc ctt ggc atg aaa tgc acc agg tgc acg ggg gac aat gag aag gtg      514
Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val
                                   100      105      110
aag gct cac att ctg ctg acg gct gga atc atc ttc atc atc acg ggc      562
Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly
                                   115      120      125      130
atg gtg gtg ctc atc cct gtg agc tgg gtt gcc aat gcc atc atc aga      610
Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg
                                   135      140      145
gat ttc tat aac tca ata gtg aat gtt gcc caa aaa cgt gag ctt gga      658
Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
                                   150      155      160
gaa gct ctc tac tta gga tgg acc acg gca ctg gtg ctg att gtt gga      706
Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly
                                   165      170      175
gga gct ctg ttc tgc tgc gtt ttt tgt tgc aac gaa aag agc agt agc      754
Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser
                                   180      185      190
tac aga tac tcg ata cct tcc cat cgc aca acc caa aaa agt tat cac      802
Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
                                   195      200      205      210
acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg      847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
                                   215      220      225
tagttgtgta tgttttttta actttactat aaagccatgc aaatgacaaa aatctatatt      907
acttttctcaa aatggacccc aaagaaactt tgatttactg ttcttaactg cctaatttta      967
attacaggaa ctgtgcatca gctatttatg attctataag ctatttcagc agaatgagat      1027
attaaaccca atgctttgat tgttctagaa agtattgtaa tttgttttct aagggtgggttc      1087
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aagcatctac tctttttatc atttacttca aaatgacatt gctaaagact gcattattct 1147
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tac cag gat ttc tat gca ttc gac ctg tca gga gcc act cga gtc ctt 97
Tyr Gln Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu
15 20 25 30
gaa tgg att gat gac aaa gga gtc ttt gtt gct ggc tat gaa agc ctg 145
Glu Trp Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu
35 40 45
aaa aag aat gaa att ctt cat ctg aaa tta cct ctc aga ctt tct gta 193
Lys Lys Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val
50 55 60
aag gaa aac aag ggc tta ttc cca gaa aga gat ttc aaa gtg cgc cat 241
Lys Glu Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His
65 70 75
gga gga ttt tca gac agg tct atc ttt gat cta aag cat gtg cca cat 289
Gly Gly Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His
80 85 90
acc aga ttg ctg gtt acc agt ggc ctt cca ggt tgt tat ctg cag gtg 337
Thr Arg Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val
95 100 105 110
tgg cag gtt gca gag gac agt gat gtc att aaa gct gtc agc acc att 385
Trp Gln Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile
115 120 125
gct gtg cat gag aaa gag gag agt ctc tgg cct agg gtg gcc gtc ttc 433
Ala Val His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe
130 135 140
tcc aca ttg gca ccc gga gtc ctc cat ggg gcg agg ctc cga agt ctg 481
Ser Thr Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu
145 150 155

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Gln Val Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val	
160 165 170	
agt gac agt gag gag ctg agt agc ctg cag gtc cta gat gcg gac acc	577
Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr	
175 180 185 190	
ttt gcc ttc tgc tgt gct tcg ggc cgg ctg ggg ctt gtt gac acc cgg	625
Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg	
195 200 205	
cag aag tgg gca ccg ttg gag aat cgc agc cct ggc cct ggg tct ggt	673
Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly	
210 215 220	
gga gag aga tgg tgt gct gaa gtt ggg agc tgg ggc cag ggc cct ggg	721
Gly Glu Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly	
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ccc agc att gcc agc ctt agc tca gat ggg cgt ctt tgt ctt ctt gac	769
Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp	
240 245 250	
ccc cgg gat ctc tgc cat cct gtg agc tca gtc cag tgc cca gta tcc	817
Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser	
255 260 265 270	
gta cct agc cct gac cca gag ctg ctg cga gtg act tgg gcc cca ggc	865
Val Pro Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly	
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Leu Lys Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val	
290 295 300	
tat gat gcc aca tct tgg gat gga aca cgg agc caa gat gga aca cgg	961
Tyr Asp Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg	
305 310 315	
agc caa gta gaa cct ctc ttc act cac aga ggt cac atc ttc cta gat	1009
Ser Gln Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp	
320 325 330	
gga aat ggg atg gac cct gct cct ttg gtc acc acc cac acc tgg cat	1057
Gly Asn Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His	
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Pro Cys Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu	
355 360 365	
cat gtg tgg gac tgg gtg gac ctt tgt gcc ccc cgc tgacaccagc	1151
His Val Trp Asp Trp Val Asp Leu Cys Ala Pro Arg	
370 375	
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<213> Homo sapiens

<220>

<221> CDS

<222> 136..264

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tcatcccaga ggata atg gca acc cat gcc tta gaa atc gct ggg ctg ttt      171
                Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe
                1             5             10
ctt ggt ggt gtt gga atg gtg ggc aca gtg gct gtc act gtc atg cct      219
Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro
                15             20             25
cag tgg aga gtg tcg gcc ttc att gaa aac aac atc gtg gtt ttt      264
Gln Trp Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
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tgcaaaaatct atgattccct gctggctctt tctccggacc tacaggcagc cagaggactg      384
atgtgtgctg cttccgtgat gtccttcttg gctttcatga tggccatcct tggcatgaaa      444
tgcaccaggt gcacggggga caatgagaag gtgaaggctc acattctgct gacggctgga      504
atcatcttca tcatcacggg catggtggtg ctcacccctg tgagctgggt tgccaatgcc      564
atcatcagag atttctataa ctcaatagtg aatggtgccc aaaaacgtga gcttggagaa      624
gctcttact taggatggac cacggcactg gtgctgattg ttggaggagc tctgttctgc      684
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acaacccaaa aaagtatatca caccggaaag aagtcaccga gcgtctactc cagaagtcag      804
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tgc ggc cag gcg tgg ggt gcg tcg gtg ggc ggc cgc agc tgc gag gag      97
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Cys	Gly	Gln	Ala	Trp	Gly	Ala	Ser	Val	Gly	Gly	Arg	Ser	Cys	Glu	Glu	
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ctc	act	gcg	gtc	cta	acc	ccg	ccg	cag	ctc	ctc	gga	cgc	agg	ttt	aac	145
Leu	Thr	Ala	Val	Leu	Thr	Pro	Pro	Gln	Leu	Leu	Gly	Arg	Arg	Phe	Asn	
	30					35					40					
ttc	ttt	att	caa	caa	aaa	tgc	gga	ttc	aga	aaa	gca	ccc	agg	aag	gtt	193
Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val	
45					50					55					60	
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggt	gaa	gca	tac	aag	aga	241
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg	
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agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
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tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	ggt	ggg	ttt	337
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe	
		95					100					105				
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg	385
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu	
	110				115						120					
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggt	ata	aaa	gct	gat	tgg	ttg	433
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu	
125					130					135					140	
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn	
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Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
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ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu	
		175					180					185				
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val	
	190					195					200					
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
205					210					215					220	
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile	
				225					230					235		
gtg	aac	att	ctg	ggt	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala	
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ggt	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggt	aaa	gtt	gcc	aca	gga	817
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly	
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aga	tat	gga	cca	tca	ctt	ggt	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met	
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gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala	
285					290					295					300	
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggt	cat	961
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His	
				305					310					315		
gaa	ctg	att	tgg	aag	aac	agg	gag	ccg	cta	gtg	aaa	atc	tgg	cat	gaa	1009
Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu	

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ata agg act aat ggc ccc aaa aaa gga ggt ggc tct aag taaaaactggg						1058
Ile Arg Thr Asn Gly Pro Lys Lys Gly Gly Gly Ser Lys						
	335		340		345	
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Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser	
1 5 10	
tgc gtg gca ggg cct gac tgc tgc gga ggc ctc ggc aat att gat ttt	159
Ser Val Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe	
15 20 25 30	
aga cag gca gac ttc tgc gtt atg acc cgg ctg ctg ggc tac gtg gac	207
Arg Gln Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp	
35 40 45	
ccc ctg gat ccc agc ttt gtg gct gcc gtc atc acc atc acc ttc aat	255
Pro Leu Asp Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn	
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ccg ctc tac tgg aat gtg gtt gca cga tgg gaa cac aag acc cgc aag	303
Pro Leu Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys	
65 70 75	
ctg agc agg gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc	351
Leu Ser Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser	
80 85 90	
atc acc atc ctg ctc ctg aac ttc ctg cgc tgc cac tgc ttc acg cag	399
Ile Thr Ile Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln	
95 100 105 110	
gcc atg ctg agc cag ccc agg atg gag agc ctg gac acc ccc gcg gcc	447
Ala Met Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala	
115 120 125	
tac agc ctg gtc ctc gca ctc ctg gga ctg ggc gtc gtg ctc gtg ctc	495
Tyr Ser Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu	
130 135 140	
tcc agc ttc ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac	543
Ser Ser Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr	
145 150 155	
ttc ggg atc ctc aag gag gcg aga gtg acc gtg ttc ccc ttc aac atc	591
Phe Gly Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile	
160 165 170	
ctg gac aac ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg	639
Leu Asp Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp	
175 180 185 190	
gcc atc atg cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg	687
Ala Ile Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val	

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Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala
210          215          220
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Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser
225          230          235
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caggccctgc gcagggcgag aatggtgcct gctgctcagg gctcgcccc ggcgtgggct      897
gccccagtgc cttggaacct gctgccttgg ggacctgga cgtgccgaca tatggccatt      957
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Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg
10          15          20
caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat      151
Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn
25          30          35
tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg      199
Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu
40          45          50
gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct      247
Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala
55          60          65          70
ggg gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat      295
Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His
75          80          85
cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg      343
Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met
90          95          100
ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt      391
Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val
105          110          115
ata acc atc tgaccagcaa ccgaagaaag ccacacaaaa aaatgtatac      440
Ile Thr Ile
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 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
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 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
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 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
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				1 5		
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Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val						
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Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro						
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ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc						318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu						
		40		45	50	
cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg						366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu						
		55		60	65	
gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct						414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala						
		70		75	80	85
gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac						462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp						
		90		95	100	
aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc						510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser						
		105		110	115	
ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa						558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln						
		120		125	130	
ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg						606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala						
		135		140	145	
ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta						654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu						
		150		155	160	165
ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg						702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met						
		170		175	180	
tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc						750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly						
		185		190	195	
cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc						798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala						
		200		205	210	
gaa ttg gac tac ctc atg gat gtg ctg gtg ggc aca cag gca ctg gag						846
Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu						
		215		220	225	
cga ccg ccg ggg cca ggg cgc tgagccctcg tgctggaatg gttgtctggt						897
Arg Pro Pro Gly Pro Gly Arg						
		230		235		
atctgaactg agcctgctgg ctggaccaac tgcctcga aagacacagc tggcttcct						957
agtacagaga acagggcttg ggccactttg gagagacaga atctagtcct gggcaacttc						1017
acatccgtcc tctgtctca gggctggcag ggggagcctg gaattacccc ctagtgatgg						1077

aatgacaggg tctggtgggg acttaattcc ctggccctgg ggtcatagct tgggctgttc 1137
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<210> 172

<211> 1487

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..640

<400> 172

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 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
 1 5 10
 ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat 157
 Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp
 15 20 25 30
 aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat 205
 Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn
 35 40 45
 aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt 253
 Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val
 50 55 60
 ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca 301
 Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser
 65 70 75
 ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct 349
 Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser
 80 85 90
 gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg 397
 Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu
 95 100 105 110
 gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att 445
 Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile
 115 120 125
 cgg gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc 493
 Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu
 130 135 140
 tct cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt 541
 Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly
 145 150 155
 aca ata gct att cag tta gca cat cat aga gga gcc aaa gta ttt caa 589
 Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln
 160 165 170
 cag cat gca gcc ttg aag ata agc agt gcc ttg aaa gat tca gac ctc 637
 Gln His Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu
 175 180 185 190
 cca tagcccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc 690
 Pro
 tgtttggaag aaacaggtgg cctgggagta gatattgtcc tagatgctgg agtgagatta 750
 tatagtaaag atgatgaacc agctgtaaaa ctacaactac taccacataa acatgatatc 810
 atcacacttc ttggtgttgg aggccactgg gtaacaacag aagaaaacct tcagttggat 870
 cctccagata gccactgcct tttcctcaag ggagcaacgt tagctttcct gaatgatgaa 930
 gtttgggaatt tgtcaaagt acaacaggga aaatatcttt gtatcttaaa ggatgtgatg 990

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ttttaattttt cttcttttctc agacctcagt cggatgaaca tattccagta tttgaagcca 1170
gaatttttctt tggaaattgt tgagaaaaac caaggaagat aaaacaagtt gcattttttaa 1230
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ccttttcatt gtttctatat attttgcccc tgctataaaa ttccttccat gaagaaaact 1410
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aaaaaaaaaa aaaaaaaa 1487

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<210> 173
 <211> 1915
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 132..1298

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<400> 173
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tgacggggaca cagtggttgg tgacggggaca gagcggtcgg tgacagcctc aagggttca 120
gcaccgcgcc c atg gca gag cca gac ccc tct cac cct ctg gag acc cag 170
          Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln
              1              5              10
gca ggg aag gtg cag gag gct cag gac tca gat tca gac tct gag gga 218
Ala Gly Lys Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly
          15          20          25
gga gcc gct ggt gga gaa gca gac atg gac ttc ctg cgg aac tta ttc 266
Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe
          30          35          40          45
tcc cag acg ctc agc ctg ggc agc cag aag gag cgt ctg ctg gac gag 314
Ser Gln Thr Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu
          50          55          60
ctg acc ttg gaa ggg gtg gcc cgg tac atg cag agc gaa cgc tgt cgc 362
Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg
          65          70          75
aga gtc atc tgt ttg gtg gga gct gga atc tcc aca tcc gca ggc atc 410
Arg Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile
          80          85          90
ccc gac ttt cgc tct cca tcc acc ggc ctc tat gac aac cta gag aag 458
Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys
          95          100          105
tac cat ctt ccc tac cca gag gcc atc ttt gag atc agc tat ttc aag 506
Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys
          110          115          120          125
aaa cat ccg gaa ccc ttc ttc gcc ctc gcc aag gaa ctc tat cct ggg 554
Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly
          130          135          140
cag ttc aag cca acc atc tgt cac tac ttc atg cgc ctg ctg aag gac 602
Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp
          145          150          155
aag ggg cta ctc ctg cgc tgc tac acg cag aac ata gat acc ctg gag 650
Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu
          160          165          170
cga ata gcc ggg ctg gaa cag gag gac ttg gtg gag gcg cac ggc acc 698
Arg Ile Ala Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr
          175          180          185

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ttc tac aca tca cac tgc gtc agc gcc agc tgc cgg cac gaa tac ccg	746
Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro	
190 195 200 205	
cta agc tgg atg aaa gag aag atc ttc tct gag gtg acg ccc aag tgt	794
Leu Ser Trp Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys	
210 215 220	
gaa gac tgt cag agc ctg gtg aag cct gat atc gtc ttt ttt ggt gag	842
Glu Asp Cys Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu	
225 230 235	
agc ctc cca gcg cgt ttc ttc tcc tgt atg cag tca gac ttc ctg aag	890
Ser Leu Pro Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys	
240 245 250	
gtg gac ctc ctc ctg gtc atg ggt acc tcc ttg cag gtg cag ccc ttt	938
Val Asp Leu Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe	
255 260 265	
gcc tcc ctc atc agc aag gca ccc ctc tcc acc cct cgc ctg ctc atc	986
Ala Ser Leu Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile	
270 275 280 285	
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Asn Lys Glu Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met	
290 295 300	
ggc ctc gga gga ggc atg gac ttt gac tcc aag aag gcc tac agg gac	1082
Gly Leu Gly Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp	
305 310 315	
gtg gcc tgg ctg ggt gaa tgc gac cag ggc tgc ctg gcc ctt gct gag	1130
Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu	
320 325 330	
ctc ctt gga tgg aag aag gag ctg gag gac ctt gtc cgg agg gag cac	1178
Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His	
335 340 345	
gcc agc ata gat gcc cag tgc ggc ggc gtc ccc aac ccc agc act	1226
Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr	
350 355 360 365	
tca gct tcc ccc aag aag tcc ccg cca cct gcc aag gac gag gcc agg	1274
Ser Ala Ser Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg	
370 375 380	
aca aca gag agg gag aaa ccc cag tgacagctgc atctcccagg cgggatgccg	1328
Thr Thr Glu Arg Glu Lys Pro Gln	
385	
agctcctcag ggacagctga gcccacaccg ggccctggccc cctctttaacc agcagttctt	1388
gtctggggag ctccagaacat ccccacatct cttacagctc cctccccaaa actgggggtcc	1448
cagcaaccct ggcccccaac ccagacaaat ctctaaccac tccagagggc caaggcttaa	1508
acaggcatct ctaccagccc cactgtctct aaccactcct gggctaagga gtaacctccc	1568
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agggagcttc gggccccccac tctgtctcct gccccgggg gctgtgggt aagtaaacca	1688
tacctaacct accccagtgt ggggtgtgggc ctctgaatct aaccacacac cagcgtaggg	1748
ggagtctgag ccgggagggc tcccagagtct ctgccttcag ctcccaaagt ggggtggggg	1808
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<210> 174

<211> 1990

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 259..1701

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 tatctgtctg agcagtggaa tgtgccagga aagaaggagc aaccactgac tgatgaacct 180
 ttgccagtct cccctccaag agggatgcc aagccttctg taagctcctc agatgtcact 240
 ggtatctagg caacaggg atg agc ctg aac ctc cct gag gcc agc tta ctt 291
 Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu
 1 5 10
 agc aga gca tcc tgg cca gaa caa gcc aag gag cca aga cga gag gga 339
 Ser Arg Ala Ser Trp Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly
 15 20 25
 cac acg gac aaa caa cag aca gaa gac gta ctg gcc gct gga ctc cgc 387
 His Thr Asp Lys Gln Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg
 30 35 40
 tgc ctc ccc cat ctc ccc gcc atc tgc gcc cgg agg atg agc cca gcc 435
 Cys Leu Pro His Leu Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala
 45 50 55
 ttc agg gcc atg gat gtg gag ccc cgc gca aaa ggc gtc ctt ctg gag 483
 Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu
 60 65 70 75
 ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc ttc aat 531
 Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg Phe Asn
 80 85 90
 gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag ttc tac 579
 Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr
 95 100 105
 gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac aaa ggt 627
 Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly
 110 115 120
 gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg tgt cta 675
 Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu
 125 130 135
 ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att gta gat 723
 Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile Val Asp
 140 145 150 155
 aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca aca aac 771
 Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Arg Trp Thr Thr Asn
 160 165 170
 aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac tgg gtg 819
 Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val
 175 180 185
 cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta gaa gaa 867
 Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu
 190 195 200
 gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act gta gag 915
 Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu
 205 210 215
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 Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser
 220 225 230 235
 atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat gca aag 1011
 Met Lys Cys His Gln Gln Glu Leu Gln Arg Met Lys Glu Asn Ala Lys
 240 245 250
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 His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg
 255 260 265
 tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga caa cat 1107

Tyr	Glu	Val	Pro	Cys	Val	Leu	Asp	Leu	Lys	Met	Gly	Thr	Arg	Gln	His		
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Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	Lys	Cys		
	285					290					295						
cag	cag	agc	aca	tct	gca	gtc	att	ggt	gtg	cgt	gtg	tgt	ggc	atg	cag	1203	
Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln		
300				305					310						315		
gtg	tac	caa	gca	ggc	agt	ggg	cag	ctc	atg	ttc	atg	aac	aag	tac	cat	1251	
Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His		
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Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe		
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ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt	gaa	ctc	ctg	ggc	cct	gtg	ctc	1347	
Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu		
		350					355						360				
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Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr		
	365					370					375						
cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc	att	tat	gat	ggc	aag	gag	cgg	1443	
Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	Glu	Arg		
380					385					390					395		
ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct	gag	gat	ttg	gag	gac	ctg	tca	1491	
Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser		
				400					405					410			
gag	gaa	tca	gct	gat	gag	tct	gct	ggt	gcc	tat	gcc	tac	aaa	ccc	atc	1539	
Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile		
			415					420					425				
ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg	atc	gac	ttt	gca	cac	acc	acc	1587	
Gly	Ala	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	Thr	Thr			
		430					435					440					
tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg	gtg	cat	gag	ggc	cag	gat	gct	1635	
Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	Asp	Ala		
	445					450					455						
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Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	Val	Thr	Glu	Ile		
460					465					470					475		
agt	gag	gag	agt	ggg	gag	tgagcttgct	agctgctcca	gtacttgaga								1731	
Ser	Glu	Glu	Ser	Gly	Glu												
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 <213> Homo sapiens

<220>
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 <222> 213..1274

<400> 175
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cctggcagaa	tcaagatgag	gccctgtcat	gcctccccag	tgaggcctac	agtctgagca	180
gacagcatgg	cctgccaactg	gcagtgaaca	cc	atg tct	gca gga ggt ggc cgg	233
				Met Ser	Ala Gly Gly Gly Arg	
				1	5	
gcc ttt gct tgg caa gtg ttc ccc ccc atg ccc act tgc cgg gtc tat	281					
Ala Phe Ala Trp Gln Val Phe Pro Pro Met Pro Thr Cys Arg Val Tyr						
10	15	20				
ggc aca gtg gca cac caa gat ggg cac ctg ctg gtg ttg ggg ggt tgt	329					
Gly Thr Val Ala His Gln Asp Gly His Leu Leu Val Leu Gly Gly Cys						
25	30	35				
ggc cgg gct gga ctg ccc ctg gac act gct gag aca ctg gac atg gcc	377					
Gly Arg Ala Gly Leu Pro Leu Asp Thr Ala Glu Thr Leu Asp Met Ala						
40	45	50	55			
tcg cac aca tgg ctg gca ctg gca ccc ctg ccc act gcc cgg gct ggt	425					
Ser His Thr Trp Leu Ala Leu Ala Pro Leu Pro Thr Ala Arg Ala Gly						
60	65	70				
gca gct gcg gta gtt ctg ggc aag cag gtg cta gtg gtg ggt ggt gtg	473					
Ala Ala Ala Val Val Leu Gly Lys Gln Val Leu Val Val Gly Gly Val						
75	80	85				
gat gag gtc cag agc ccg gta gct gct gta gag gcc ttc ctg atg gat	521					
Asp Glu Val Gln Ser Pro Val Ala Ala Val Glu Ala Phe Leu Met Asp						
90	95	100				
gag ggc cgc tgg gag cgt cgg gcc acc ctc cct caa gca gcc atg ggg	569					
Glu Gly Arg Trp Glu Arg Arg Ala Thr Leu Pro Gln Ala Ala Met Gly						
105	110	115				
gtt gca act gtg gag aga gat ggt atg gtg tat gct ctg ggg gga atg	617					
Val Ala Thr Val Glu Arg Asp Gly Met Val Tyr Ala Leu Gly Gly Met						
120	125	130	135			
ggc cct gac acg gcc ccc cag gcc cag gta cgt gtg tat gag ccc cgt	665					
Gly Pro Asp Thr Ala Pro Gln Ala Gln Val Arg Val Tyr Glu Pro Arg						
140	145	150				
cgg gac tgc tgg ctt tcg cta ccc tcc atg ccc aca ccc tgc tat ggg	713					
Arg Asp Cys Trp Leu Ser Leu Pro Ser Met Pro Thr Pro Cys Tyr Gly						
155	160	165				
gcc tcc acc ttc ctg cac ggg aac aag atc tat gtc ctg ggg ggc cgc	761					
Ala Ser Thr Phe Leu His Gly Asn Lys Ile Tyr Val Leu Gly Gly Arg						
170	175	180				
cag ggc aag ctc ccg gtg act gct ttt gaa gcc ttt gat ctg gag gcc	809					
Gln Gly Lys Leu Pro Val Thr Ala Phe Glu Ala Phe Asp Leu Glu Ala						
185	190	195				
cgt aca tgg acc cgg cat cca agc cta ccc agc cgt cgg gcc ttt gct	857					
Arg Thr Trp Thr Arg His Pro Ser Leu Pro Ser Arg Arg Ala Phe Ala						
200	205	210	215			
ggc tgc gcc atg gct gaa ggc agc gtc ttt agc ctg ggt ggc ctg cag	905					
Gly Cys Ala Met Ala Glu Gly Ser Val Phe Ser Leu Gly Gly Leu Gln						
220	225	230				
cag cct ggg ccc cac aac ttc tac tct cgc cca cac ttt gtc aac act	953					
Gln Pro Gly Pro His Asn Phe Tyr Ser Arg Pro His Phe Val Asn Thr						
235	240	245				
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Val Glu Met Phe Asp Leu Glu His Gly Ser Trp Thr Lys Leu Pro Arg						
250	255	260				
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Ser Leu Arg Met Arg Asp Lys Arg Ala Asp Phe Val Val Gly Ser Leu						
265	270	275				
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Gly Gly His Ile Val Ala Ile Gly Gly Leu Gly Asn Gln Pro Cys Pro						

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ttg cct gcc atg ccc act gcc cgc tgc tcc tgc tct agt ctg cag gct 1193
Leu Pro Ala Met Pro Thr Ala Arg Cys Ser Cys Ser Ser Leu Gln Ala

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ggg ccc cgg ctg ttt gtt att ggg ggt gtg gcc cag ggc ccc agt caa 1241
Gly Pro Arg Leu Phe Val Ile Gly Gly Val Ala Gln Gly Pro Ser Gln

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gcc gtg gag gca ctg tgt ctg cgt gat ggg gtc tgaaggcttg gtgggagctg 1294
Ala Val Glu Ala Leu Cys Leu Arg Asp Gly Val

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Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
1 5 10
ata aca ttt gta ttt caa taaaaggaag atcttctctgt tacagaggat 157
Ile Thr Phe Val Phe Gln
15 20
aactttgtga aacttcaagt taaagcttgt gctctgagcc agataaatac aaagcttctg 217
gcagaaatga agatgaaaaa ggatttattt cctgttgga gagaaattgc tggaattgta 277
ttagatgttg gaagcaaggt atcattcctt caaccagatg atgaagtagt tggaattttg 337
cccctggact ctgaagaccc tggactttgt gaagttgtta gagtacatga gcattacttg 397
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Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile
1 5 10 15
aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat aac 157
Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn
20 25 30
ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat aca 205
Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr
35 40 45
aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt ggg 253
Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly
50 55 60
aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca ttc 301
Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe
65 70 75
ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct gaa 349
Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu
80 85 90 95
gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg gtt 397
Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val
100 105 110
cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att cgg 445
His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg
115 120 125
gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc tct 493
Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser
130 135 140
cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt aca 541
Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr
145 150 155
ata gct att cag tta gca cat cat aga gga gcc aaa gtg att tca aca 589
Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Ile Ser Thr
160 165 170 175
gca tgc agc ctt gaa gat aag cag tgc ctt gaa aga ttc aga cct ccc 637
Ala Cys Ser Leu Glu Asp Lys Gln Cys Leu Glu Arg Phe Arg Pro Pro
180 185 190

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195 200 205	
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Ser Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp	
210 215 220	
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Ala Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu	
225 230 235	
caa cta cta cca cat aaa cat gat atc atc aca ctt ctt ggt gtt gga	829
Gln Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly	
240 245 250 255	
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Gly His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp	
260 265 270	
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Ser His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp	
275 280 285	
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Glu Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu	
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Lys Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val	
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Met Glu Lys	
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ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag ggc ctg act	165
Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln Gly Leu Thr	
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Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr Arg Leu Lys	
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Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser Ile Leu Gly	
40 45 50	
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Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe	

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Tyr Thr Leu		Gly Asn Leu Ala		Leu Ala Ser Thr		Cys Phe Leu Met	
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gga cct gtg		aag caa ctg aag		aaa atg ttt gaa		gca aca aga ttg ctt	405
Gly Pro Val		Lys Gln Leu Lys		Lys Met Phe Glu		Ala Thr Arg Leu Leu	
	85		90		95		
gca aca att		gtt atg ctt ttg		tgt ttc ata ttt		acc ctg tgt gct gct	453
Ala Thr Ile		Val Met Leu Cys		Phe Ile Thr Leu		Cys Ala Ala	
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ctt tgg tgg		cat aag aag gga		ctg gct gtg tta		ttc tgc ata ttg cag	501
Leu Trp Trp		His Lys Lys Gly		Leu Ala Val Leu		Phe Cys Ile Leu Gln	
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Phe Leu Ser		Met Thr Trp Tyr		Ser Leu Ser Tyr		Ile Pro Tyr Ala Arg	
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Asp Ala Val		Ile Lys Cys Cys		Ser Ser Leu Leu		Ser	
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cgg gcg gcg		cgg aaa cg		gcg ggt ctg		gcg gcc caa ccc	100
Arg Ala Ala		Arg Lys Arg		Ala Gly Leu		Ala Ala Gln Pro	
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agt cag ggc		gca caa acc		cca gga gag		aag gcg gaa gca	148
Ser Gln Gly		Ala Gln Thr		Pro Gly Glu		Lys Ala Glu Ala	
	25		30		35		40
cta aag gca		gcc cca ggc		tgg cta aag		cgg ttc ctg gta	196
Leu Lys Ala		Ala Pro Gly		Trp Leu Lys		Arg Phe Leu Val	
		45		50		55	
agg ccc gcg		agt gcc cg		gcg gcc cag		ccc ggc cta gtt	244
Arg Pro Ala		Ser Ala Arg		Ala Gln Pro		Gly Leu Val Gln	
	60		65		70		
cag ccc cag		ggc agc aca		tca gag aca		cca tgg aac	292
Gln Pro Gln		Gly Ser Thr		Ser Glu Thr		Pro Trp Asn Thr	
	75		80		85		
ctg ccg tgc		tgg gac cag		tct ttc ctg		acc aat atc	340
						acc ttc ttg	

Leu	Pro	Ser	Cys	Trp	Asp	Gln	Ser	Phe	Leu	Thr	Asn	Ile	Thr	Phe	Leu		
90						95					100						
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Lys	Val	Leu	Leu	Trp	Leu	Val	Leu	Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu		
105						110					115				120		
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Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu	Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val		
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Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys	Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr		
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Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu	Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala		
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Ser	Thr	Val	Leu	Ser	Ser	Val	Pro	Leu	Gln	Met	Leu	Phe	Tyr	Leu	Ser		
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Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp
          45                      50                      55
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Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr
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Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Leu Ser Ala His Phe Leu
          95                      100                      105
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Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr
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ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc      436
Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile
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Ala Ala Phe Thr Arg
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ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc      1391
accgcatttt gtaaataaag agatgtgtat gcctcaaaaa aaaaaaaaaa aa      1443

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<211> 605
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 232..450

<400> 181
caaatacaaa tgccccaaga agactgagga taggagaaag aatatctcta cctgtgaaac      60
attgttagac tgcctggcta ggagttcatt gttgttttct gaaggacgta accaaccact      120
ccaaaactta caggcttaaa acaacaaaca tgtatcattt cttatgattc tgtgggttgg      180
ctgggtggtt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct      237
                                   Met Ser
                                   1
ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg      285

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Gly	Val	Pro	Ala	Glu	Met	Thr	Gly	Ala	Val	Glu	Ala	Phe	Leu	Pro	Val	
		5					10				15					
gtg	tca	tcc	tcc	aga	agg	ctg	ccc	aga	ttt	gtc	cat	atg	gta	gca	gga	333
Val	Ser	Ser	Ser	Arg	Arg	Leu	Pro	Arg	Phe	Val	His	Met	Val	Ala	Gly	
	20					25				30						
gtt	tcc	tcg	aag	caa	gag	agg	gca	aga	tcc	aac	aca	gaa	gca	ctt	ttc	381
Val	Ser	Ser	Lys	Gln	Glu	Arg	Ala	Arg	Ser	Asn	Thr	Glu	Ala	Leu	Phe	
	35				40					45					50	
aag	ctc	tgt	ttc	cat	cac	att	tgc	caa	tgt	ctc	act	gat	gaa	cac	aag	429
Lys	Leu	Cys	Phe	His	His	Ile	Cys	Gln	Cys	Leu	Thr	Asp	Glu	His	Lys	
				55				60						65		
ttc	cat	ggc	caa	gtc	cag	ttt	taagaaatgg	agaaaataggg	cttggtcag							480
Phe	His	Gly	Gln	Val	Gln	Phe										
		70														
tggctcatgt	ctgtaatccc	agcacttttg	gaggccaagg	catgcggatc	atttgaggtc											540
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aaaaa																605
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ccagcccccc	accatggtaa	gtccttca	ag	ggtgggatct	ggaagagg	aa	agaggagg	ga								180
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cttaccagg	agcaagctcc	catctgtagg	tg	ggtggggat	gccagggtg	g	tatccctgga									360
tccaaggata	gggcaggacc	tggaagacag	aagg	tggccc	aggagaatc	acagag	ctctg									420
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tcccacagat	gtcatatttg	gaaatccgtc	tagatgcgga	agttgctctt	caggggtctt											600
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atggctgcag	cagaggcagg	agaggctgaa	tacgtcc	atg cca	ccc ttt	ggt ggg										775
				Met	Pro	Pro	Phe	Gly	Gly							
cat	ccc	tta	tcc	caa	gag	gag	gat	ggc	agc	cag	agg	tgt	tgc	tgc	ctg	823

ggc tgt gac agc ggc cac tgc agg att ctt ggc agg tac agc tta cta 1063
 Gly Cys Asp Ser Gly His Cys Arg Ile Leu Gly Arg Tyr Ser Leu Leu
 90 95 100

ggg tgg agt cag gga cat agg gca aga ggc aga ggt ggt gtt agt ctg 1111
 Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu
 105 110 115

aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg 1159
 Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
 120 125 130

ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag 1213
 Leu Met Pro Val Ile Pro Ala Phe
 135 140

gtcaggtggt cgagaccagc ctggccaacg tgggtgaaacc tcgtctctac taaaaaatac 1273
 aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg 1333
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 ggcaccccg aattcacacc caaacatca gctggagctc tgagactggt ggggtgggaa 1513
 ttcttccaag atgagaagca agccaggag gctcaggtcc tgggatgggc agggctttga 1573
 tcaaaagaac acaggaagtg atttgctact tgaaagaaag gcaaccctc cccaaggaag 1633
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 <222> 486..932

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 atggggtttc accatgttgg ccaggctggc cttgaactcc tgacctcagg tgatccgccc 180
 gcctcggcct cccaaagtgc tggggttaca ggcagtagcc accgcacccg gcccccttc 240
 ttcgtcttag tcaatcctat cccacctctt ctccaccag tccctcacc tgatgggtccc 300
 aacacttcat catccaccac ctccctggagg gggtagcccg aggtgctccg ctgggggactc 360
 tgctcattct ggggggtgcag ttgacggctg gtcgtgatct ttcccgtaat ctgtcccctc 420
 ttacggaacc tagtctccgt tctgtccatg gccttcttct ggacactgct aggatccaga 480
 agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca 530
 Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
 1 5 10 15

gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt 578
 Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
 20 25 30

ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat 626
 Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
 35 40 45

gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct 674
 Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
 50 55 60

gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt 722
 Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
 65 70 75

ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc 770
 Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
 80 85 90 95

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ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
          100          105          110
gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc      866
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
          115          120          125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc      914
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
          130          135          140
aga aac gat gaa acc tta taagagtga attatcatgt gcaagagtga      962
Arg Asn Asp Glu Thr Leu
          145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag      1022
cactcagttt tggcagagct ttttctgccg aatgtttact cacattcact gtccgagatt      1082
ctatactggg ggtacacacg tcctctgccg taaggcaatt ttgagtccaa gagacatttt      1142
gaggcctaaa aatcatagga aactgcccct gagctcacac atatttccaa tgggtgtcccc      1202
aatctcaggg aatccatgga ttacctaagc cagcccctcc agttcggcta agaaactcta      1262
gtctatatgt caagttttgt atcatatgta ttgctctgaa ctcagaaaatt tcccttccat      1322
ttatggattc tatgaataaa atatcacatg tacaaaaaga ctaagtcaaa aaatttcagc      1382
tgtgcacagt ggctcatgct tgtaatccca gcactttggg tggccgaggg gggaggattg      1442
cctgaggcca gcagttcaag accagtatgg gcaacatggc aagagcccat ctctaaaaaa      1502
acaaaaccaa accaaattgg ccaggtgtgg tggctggcac ctgtgttcca actacttggg      1562
agactcatgt gacaggaaga tcacttgagc ccggggggtta gaggctgcag tgagctatga      1622
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aaaa

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<210> 184
<211> 463
<212> DNA
<213> Homo sapiens

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<222> 80..304

<400> 184

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ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc      112
          Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys
          1          5          10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg      160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu
          15          20          25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc      208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
          30          35          40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg      256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
          45          50          55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac      304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
          60          65          70          75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt      364
gtcctgtttc ccccttttta attttatccc ttgctagaat taagatacta tatgacctcac      424
ttatcaatta cagtctaaat ccaaaagaaa aaaaaaaaaa      463

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<210> 185
<211> 773

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 188..691

<400> 185
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tacagtaaca atggcagcct ttttgttgct gggacatcca tacaggcaac ttagctgggtg 120
aaaggactct ggattggttg gcagtcctgct tttttttttc caaggtgata actttactgt 180
agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229
Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys
1 5 10
ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277
Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln
15 20 25 30
cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325
Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp
35 40 45
aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373
Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr
50 55 60
tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421
Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr
65 70 75
gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469
Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr
80 85 90
cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517
Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His
95 100 105 110
tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565
Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His
115 120 125
ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613
Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr
130 135 140
att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt 661
Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Leu
145 150 155
ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa 711
Phe Ile Ile Val Phe Ile Leu Ile Phe Phe
160 165
acagcaatga gcatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 771
aa 773

<210> 186
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 94..573

<400> 186
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catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc      114
                               1       5
cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
                               10      15      20
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag      210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
                               25      30      35
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
40                               45      50      55
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
                               60      65      70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
                               75      80      85
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg      402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp
                               90      95      100
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga      450
Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly
105                               110      115
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat      498
Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His
120                               125      130      135
tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca      546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro
140                               145      150
ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca      593
Gly Gly Gly Ile Pro Gly Pro Trp His
155                               160
agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga      653
attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt      713
tataaagctc tccccaaacc gtgttaaaaa aaaaaaaaaa      753

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<210> 187

<211> 754

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 181..462

<400> 187

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attgagttat tacatatcaa ttgaacaagg tagttttaaa atgaaagaaa atcttgcaac      180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc      228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
1                               5      10      15
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct      276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
20                               25      30
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga      324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg

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      35              40              45
ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg      372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro
      50              55              60
tcc gcc ctc cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg      420
Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
      65              70              75              80
agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc      462
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser
      85              90
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca      522
tagctctgtg ccttgctggg gtctgaggtt cacagggtcag atgctgctgt ctggtccttc      582
ccaattgcgg cgtgaattcc ttcacacctca ccagtagctt cttgctctcc ccaaggagg      642
cacgtgctta gtagggagag aggcctacca aggttgccat ctgccatggg ctcaattgtg      702
tccccaaccc ccttgcaaat tatatattga agtcccaaaa aaaaaaaaaa aa      754

<210> 188
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<212> DNA
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<220>
<221> CDS
<222> 6..290

<220>
<221> misc_feature
<222> 871
<223> n=a, g, c or t

<400> 188
gattc atg aag gcc tcg ggt cct gac ctc tct gat gga ctc cac tgc ccc      50
Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro
      1              5              10              15
agt cta att aga cat tta aga acc ttc tct gca gct gct gcc tta gcc      98
Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala
      20              25              30
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc      146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu
      35              40              45
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc      194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser
      50              55              60
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca      242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr
      65              70              75
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat      290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
      80              85              90              95
taaagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc cagggagggc      350
tttgtccttg acaatcccac tgacttattt aacaggtagc tcaaaaccca acaaaaactg      410
gaggaggctg ctccactgca gggatgggtt caattcggtg actggagtat tgtactctcc      470
ttgcaccttg gctcatcccc acaaaaagacc tttcaaagaa aacacttaat tacctccttg      530
cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaagggtc acagagaagg      590
agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc      650
tgccacctcc taggaagcta aaagaattaa ggggaggccg ggcacgggtg ctcacgcctg      710
taatcccagc actttgggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca      770
tcctggctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccgggcgtg      830

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cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag	143
Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys	
35 40 45	
gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tgc gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	
gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcgagtca gcaggggccg	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgcccccg ccagaacggg cagggctgcc actgacctga agactccgga ctgggacccc	448
actccgaggg cagctcccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa	508
ataaaaaaaaa aaaaaaaaa	526
<210> 191	
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<222> 174..527	
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cccatcaccg ccacagaccc ccagcccttc agttgccctg cacctccttg gtg atg	176
Met	
1	
cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
5 10 15	
tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
20 25 30	
tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
35 40 45	
ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa	368
Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
50 55 60 65	
aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga	416
Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
70 75 80	
gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt	464
Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
85 90 95	
gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
100 105 110	

agg act tcc tcc ctc taaggagctc cccataccccc ccatcacctt ggcattccca 567
Arg Thr Ser Ser Leu

115

gctcctccag aatccctccc tcctcagcc tagagaagga caactgcttc cccttggggc 627
ttgtcccttc acctccttga ggaaagaact gggagtaaact ctgcttgaag ttctcctcat 687
tgacaattcc gctgggacat tcctggaagg agagggcacc aggctgaggg cagagacaaa 747
atcccccttc gttcaccgcc cccaccctcc atggcccaag actcccaggg agggggataa 807
tcttcaagcc tccagaggac tcaccacgtg gctcatgtga tgggagggaa gacttctttc 867
ccagtgcaca aataaaaaaac atggaacgaa aaaaaaaaaa aaa 910

<210> 192

<211> 668

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..203

<400> 192

tcctgtcgac gtgttcttcc ggtggcggag cggcggatta gccttcgcgg ggcaaa atg 59
Met

1

gag ctc gag gcc atg agc aga tat acc agc cca gtg aac cca cct gtc 107
Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro Val

5

10

15

ttc ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc 155
Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr

20

25

30

gcc tgg ttc ttc gtg tat cct ttc act gag cag cca gag gac cag cat 203
Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln His

35

40

45

tagtgatgtg ggaagctcag ggagaaacca cgctaggtac atggaccccg ccggttttgt 263
acattggatt ggggctgaga gaagattgcc gtgggctggg ctctctgcac tccacagtcc 323
acccttctgc tttgccttaa ctgctgtgcc cagttacgag gtcacctcta ccaagtacac 383
tcgtgatatc tataaagagc tcctcatctc attagtggcc tcactcttca tgggcttttg 443
agtcctcttc ctgctgtctc gggttggcat ctacgtgtga gcaccaagg gtaacaacca 503
gatggcttca ctgaaacctg cttttgtaaa ttactttttt ttactgttgc tggaagtgtc 563
ccacctgctg ctcataataa atgcagatgt atagcaaaaa aaaaaaaaaa aaaaaaaaaa 623
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 668

<210> 193

<211> 637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..334

<400> 193

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cccaggc atg ctg gct ctc ttc cac ttc cac ctt cca cca tgg gat gac 109

1

5

10

gca gta aga agg cca tca gta gat gcc agt ccc tca acc ttg aac ttt 157
Ala Val Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe

15

20

25

30

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cca gac gca gaa ctt tat gcc tcc att ttc ctc tgc tgc atg gcc cca 205
Pro Asp Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro
          35          40          45
gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca 253
Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala
          50          55          60
aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc 301
Asn Gly Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val
          65          70          75
tgg cat gaa aat tca caa gaa gag agg aaa tac tgaggagaaa atggcagatt 354
Trp His Glu Asn Ser Gln Glu Glu Arg Lys Tyr
          80          85
gtgttttgctg aatttgattg acgaagaagt caccatgaaa atcacagtga accatttgga 414
aagcaaaactg ccaaaaaaat aatagttagt catgctctca ggctgggtgt tttggctgtt 474
gtgggtttct tgcatttcca gatgattgca aagagctgtt tctcaatttc tgcaacaagt 534
gccagctgaa attttggtac cagtttcatt aaatatgtat aacaaaakaa aaaaaaaaaa 594
aaaaaaaaaa aaaaaaaaaa aaaaaaagaa aaaaaaaaaa aaa 637

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<210> 194
 <211> 706
 <212> DNA
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<220>
 <221> CDS
 <222> 183..443

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<400> 194
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cacagaaacc cagggccgaa gcaaagtccc aatcccagag aggctggggc acacctacaa 120
ctgaaaggag gcttagaaaat ccttcagaga ccaccctatc ggttctctc cacctggaca 180
gg atg agc cag caa cac aga agg aag cct tcc tcc gaa aga aaa 227
Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys
1 5 10 15
agc aca aga aag atg gac aca tgg cag agt ctt aaa gtc aaa gaa gta 275
Ser Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val
20 25 30
ttc tgt aag cat aat tct tcc tat gaa tgc ctt ctc tat aaa gag gtt 323
Phe Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val
35 40 45
gaa gca aga cag gtt tct aag aca gcc acc gat ggg tcc tac ctc ctc 371
Glu Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu
50 55 60
gta ttc aca tcc tat gta atc tcc tcc cca gtg tgg act gga cct ggt 419
Val Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly
65 70 75
gac ttg ctt cca gtg aat aga ata tagcaaaagt gattgatgtc acctccaaga 473
Asp Leu Leu Pro Val Asn Arg Ile
80 85
ttcagctata gaagactatg actatgactt tcctcttggc tagcattctc gctaaccctt 533
cctgcttgct tgtactgagc tgccctatga agaggcccat gtaggggtggc ctgggtgggg 593
gtgatctgtg gccaacagcc agcaaggaac taaatcctgt ttacaaccac atgagcttgg 653
aaggagatcc ttccccagta aagccaggag atgaatacaa aaaaaaaaaa aaa 706

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<210> 195
 <211> 670
 <212> DNA
 <213> Homo sapiens

[illegible]

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<220>
<221> CDS
<222> 22..357
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[illegible]

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<210> 198
<211> 667
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 4..333

<400> 198																
aaa	atg	gtg	ttt	gga	gcc	atg	gtc	ctt	ctt	gtg	gga	ctt	gaa	gaa	ctg	48
	Met	Val	Phe	Gly	Ala	Met	Val	Leu	Leu	Val	Gly	Leu	Glu	Glu	Leu	
	1			5						10					15	
acc	aat	atc	cgc	aac	gtg	gag	aga	ctg	aag	gac	ttg	agg	gcc	agt	96	
Thr	Asn	Ile	Arg	Asn	Val	Glu	Arg	Leu	Lys	Lys	Asp	Leu	Arg	Ala	Ser	
				20					25					30		
tat	tgc	ctc	atc	gac	agc	ttc	ctg	ggg	gac	tcg	gag	ctc	atc	ggg	gac	144
Tyr	Cys	Leu	Ile	Asp	Ser	Phe	Leu	Gly	Asp	Ser	Glu	Leu	Ile	Gly	Asp	
			35					40					45			
ctg	acc	cag	tgt	gtg	gac	tgc	gtg	att	cct	cca	gag	ggg	tcc	ctc	ttg	192
Leu	Thr	Gln	Cys	Val	Asp	Cys	Val	Ile	Pro	Pro	Glu	Gly	Ser	Leu	Leu	

50	55	60	
cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct			240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro			
65	70	75	
ggt gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt			288
Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu			
80	85	90	95
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga			333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly			
100	105	110	
tgaacggttag ctgctgcggt tacattatta gcttcagttt gcccgcccag gctagatggt			393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaagtgaa			453
ggaactcagg ctccagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct			513
ggctgtgggt ttctcccat tccctgcca tctgggaagt cgctgccacc ccctacgctt			573
gtctgtgac tccagtgccc cctaaccccc cagaatgtaa acagcagcag atgaacaaaa			633
ataaaaaatac aaaaggccga aaaaaaaaaa aaaa			667
<210> 199			
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<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> 1..363			
<400> 199			
acg agt tct tcc ggg gcg gag gtc acc atg gca gct gcc ttg gct cgg			48
Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg			
1	5	10	15
ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc			96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe			
20	25	30	
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt			144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser			
35	40	45	
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg			192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val			
50	55	60	
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg			240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly			
65	70	75	80
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc			288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu			
85	90	95	
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg			336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly			
100	105	110	
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca			383
Asp Lys Pro Gly Ala Asp Thr Gly Arg			
115	120		
acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttcaact taatcattca			443
aatcactatc tgaagggtca cggagcgcaa aataaagttt aaaaccctgc taccaaaaaa			503
aaaaaaaaa a			514
<210> 200			
<211> 462			
<212> DNA			

<213> Homo sapiens

<220>

<221> CDS

<222> 41..337

<400> 200

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cttcaccacc aaaactctcc actccaccag cacagccaaa atg ctc gca cgt gct      55
                                         Met Leu Ala Arg Ala
                                         1      5
act ttc cgc gcc gcc tcg gcc cca act ctc gtc gcc cgc cgc ggc ttc      103
Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
                        10                        15                        20
cag tcg acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt      151
Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
                        25                        30                        35
cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc      199
Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
                        40                        45                        50
aag tac tgg ggc ttt atg ggc acc gga ttc gcc ctt ccc ttc ctc ctt      247
Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
                        55                        60                        65
gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg      295
Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
                        70                        75                        80                        85
gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat      337
Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
                        90                        95
taggtggagg gcccgcatcac ggctatacta gacatcacag catcaatttc attgtctgtc      397
ccccaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa
aaaaaa      457
aaaaaa      462
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<210> 201

<211> 551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..549

<400> 201

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aga gag gga gcc cga gcc agg cca tct cca acc atg tcc gac gag gcc      48
Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1      5      10      15
tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc      96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
                        20                        25                        30
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag      144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
                        35                        40                        45
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc      192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
                        50                        55                        60
cat cgc acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta      240
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
                        65                        70                        75                        80
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg      288
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Thr	Ser	Cys	Gly	Thr	Ser	Val	Ala	Ser	Ser	Glu	Gly	Ser	Glu	Glu	Leu	
				85					90					95		
ttt	tca	tct	gtg	tct	gtt	gga	gat	caa	gat	gat	tgc	tat	tcc	ctg	tta	336
Phe	Ser	Ser	Val	Ser	Val	Gly	Asp	Gln	Asp	Asp	Cys	Tyr	Ser	Leu	Leu	
			100				105						110			
gat	gat	cag	gac	ttc	act	tct	ttt	gat	tta	ttt	cct	gag	ggg	agt	gtc	384
Asp	Asp	Gln	Asp	Phe	Thr	Ser	Phe	Asp	Leu	Phe	Pro	Glu	Gly	Ser	Val	
			115				120						125			
tgc	agt	gat	gtc	tct	tct	tct	att	agc	act	tac	tgg	gat	tgg	tca	gat	432
Cys	Ser	Asp	Val	Ser	Ser	Ser	Ile	Ser	Thr	Tyr	Trp	Asp	Trp	Ser	Asp	
			130				135						140			
agc	gag	ttt	gaa	tgg	cag	tta	cca	ggc	agt	gac	att	gcc	agt	ggg	agt	480
Ser	Glu	Phe	Glu	Trp	Gln	Leu	Pro	Gly	Ser	Asp	Ile	Ala	Ser	Gly	Ser	
					150					155					160	
gat	gta	ctt	tct	gat	gtc	ata	ccc	agt	att	cca	agt	tca	cct	tgc	ctg	528
Asp	Val	Leu	Ser	Asp	Val	Ile	Pro	Ser	Ile	Pro	Ser	Ser	Pro	Cys	Leu	
					165				170					175		
ctt	cct	aaa	aaa	aaa	aaa	aa										551
Leu	Pro	Lys	Lys	Lys	Lys	Lys										
			180													

<210> 202
 <211> 550
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..315

<220>
 <221> misc_feature
 <222> 483
 <223> n=a, g, c or t

<400> 202																
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				Met	Ser	Asp	Glu	Ala	Ser	Ala						
				1				5								
atc	act	tcc	tac	gag	aag	ttt	cta	acc	ccc	gag	gag	ccc	ttc	cca	ctc	102
Ile	Thr	Ser	Tyr	Glu	Lys	Phe	Leu	Thr	Pro	Glu	Glu	Pro	Phe	Pro	Leu	
			10				15					20				
ctg	gga	cct	cct	cgc	ggg	gtg	ggc	acc	tgc	ccg	agc	gag	gag	ccg	ggc	150
Leu	Gly	Pro	Pro	Arg	Gly	Val	Gly	Thr	Cys	Pro	Ser	Glu	Glu	Pro	Gly	
		25				30					35					
tgc	ctg	gac	atc	agc	gac	ttc	ggc	tgc	cag	ctg	tcc	tcc	tgc	cat	cgc	198
Cys	Leu	Asp	Ile	Ser	Asp	Phe	Gly	Cys	Gln	Leu	Ser	Ser	Cys	His	Arg	
		40			45				50					55		
acc	gac	ccg	ctc	cac	cgc	ttc	cac	acc	aac	agg	tgg	aac	cta	act	tct	246
Thr	Asp	Pro	Leu	His	Arg	Phe	His	Thr	Asn	Arg	Trp	Asn	Leu	Thr	Ser	
				60				65					70			
tgt	gga	aca	agt	gtt	gcc	agc	tca	gaa	ggc	agt	gag	gag	ctg	ttt	tca	294
Cys	Gly	Thr	Ser	Val	Ala	Ser	Ser	Glu	Gly	Ser	Glu	Glu	Leu	Phe	Ser	
			75				80						85			
tct	gtc	tgt	tgg	aga	tca	aga	tgattgctat	tcctgttag	atgatcagga							345
Ser	Val	Cys	Trp	Arg	Ser	Arg										
				90												
cttcacttct	tttgatttat	ttcctgaggg	gagtgctctgc	agtgatgtct	cttcttctat											405

tagcacttac tgggattggg cagatagcga gtttgaatgg cagttaccag gcagtgacat 465
 tgccagtggg agtgatgnta ctttctgatg tcatacccag tattccaagt tcaccttgcc 525
 tgcttcctaa aaaaaaaaaa aaaaa 550

<210> 203
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..315

<400> 203
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 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 ctg agc gac cca gcc gcg gag cga ggt gag atg ccg gtg gcc gtg ggt 96
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 240
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 288
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105
 atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagcaaaa 395
 aaaaaaaaaa aaa 408

<210> 204
 <211> 665
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 94..582

<400> 204
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 catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
 Met Pro Arg Ser Ser Arg Ser
 1 5
 cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162
 Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
 10 15 20
 ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag 210
 Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
 25 30 35

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gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
40          45          50          55
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
60          65          70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
75          80          85
ctg ttt aac acg tgc aga tgc aag ctg tgc cag aag ctc atg gag      402
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu
90          95          100
aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct      450
Lys Thr Gly Ile Leu Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro
105          110          115
gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg      498
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg
120          125          130          135
aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg      546
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu
140          145          150
cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgaccat      592
Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys
155          160
gaaaatattg tagaagccaa gaaatgcttc agaagttata aagctctccc caaacccgcaa      652
aaaaaaaaaa aaa      665

<210> 205
<211> 1008
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 540..923

<400> 205
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agactcccgg agccctggtc tctacaccac atggacgtta tccacctcct ctgtgtcctc      120
ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cccttcaaata cegtctttgt      180
gccccactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg      240
gtctcttcgg aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc      300
cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag      360
ccccaccatg gtccttcggc ctcagcagtt ccaattctac cagccacagg ggatcacctc      420
ctccccctca gccgtggtgg tggagatggg gtccaagcct gccctcacgg gggagcccgc      480
cctcacgtgc atcagcaggg gcagtgaggc ggatecactc cgcggccagc tccctcatt      539
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg      587
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1          5          10          15
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga      635
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20          25          30
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc      683
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35          40          45
cct cct ccc acc aaa cat tac acc tcc cat ccc acc tcc gga aag cct      731
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
50          55          60

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SECRET

<213> Homo sapiens

<222> 77. .364

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaqaaaa aaaaaaaaaa a

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<213> Homo sapiens

<222> 65..544

<400> 207
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Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile
1 5 10 15
acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg 157
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met
20 25 30
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg 205
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg
35 40 45
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg 253
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met
50 55 60
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta 301
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu
65 70 75
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag 349
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys
80 85 90 95
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag 397
Thr Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln
100 105 110
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca 445
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser
115 120 125
gtg aca tta atc tgc agg aga agg act ggg act gac tat gat gaa aag 493
Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys
130 135 140
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag 541
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys
145 150 155
tgc tgatccctct tccttcccag ttgcccttaa gaactgagaa aggacaaagt 594
Cys
160
actctaagca gcagagccca cagaggctcg ttcctttgac ccttgctctcc tgggtggctat 654
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Met
1
gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg 167
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val
5 10 15
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc 215
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys

20	25	30	
agc ctg cac agc cgg gcc ttt gga ctc ctg gat gct aga gtg acc tgg			263
Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr Trp			
35	40	45	
gcg ctg agg agg gcc ccc gag cca gta cca gga aag gat aga ctc ctg			311
Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu Leu			
50	55	60	65
ctt gca gca ttc cca gca gag gca tgc cct gtg gac acc gcg tct gtg			359
Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser Val			
70	75	80	
tct gta tat ggc aga gct ccc aga tat atg cac aag gga gtg aaa aaa			407
Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys Lys			
85	90	95	
tgt gtt tgc acc cca gtc tct aaa aat tca aca gcc tgg tta ctt ctg			455
Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu Leu			
100	105	110	
ggt ggt ata tgc taggtggctt taatacgtgt tatttgcctca tctgtatttc			507
Gly Gly Ile Ser			
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		Met Cys	
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Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val Leu Ala			
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gat gtc cgc acc atc gtg aac cag atc agc tac acc ccc cag gat ccc			994
Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln Asp Pro			
20	25	30	
cga gac ctc tgt gga cgc ata ctg acc acc tgc tac atg gcc agc aag			1042
Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala Ser Lys			
35	40	45	50

aac tcc tcc cag gag acg tgc acc cgg gcc aga gag ttg gcc cag cag	1090
Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala Gln Gln	
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att gga agc cac cac atc agt ctc aac atc gat cca gcc gtg aag gcc	1138
Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val Lys Ala	
70 75 80	
gtc atg ggc atc ttc agc ctg gtg acg ggg aag agc cct ctg ttt gca	1186
Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu Phe Ala	
85 90 95	
gct cat gga gga agc agc agg gaa aac ctg gcg ctg caa aat gtg cag	1234
Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn Val Gln	
100 105 110	
gct cga ata cgg atg gtc ctc gcc tat ctg ttt gct cag ttg agc ctc	1282
Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu Ser Leu	
115 120 125 130	
tgg tct cgg ggt gtc cac ggt ggg ctc ctc ctg gga tcc gcc aac	1330
Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser Ala Asn	
135 140 145	
gtg gat gag agt ctc ctg ggc tac ctg acc aag tac gac tgc tcc agt	1378
Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser	
150 155 160	
gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc	1426
Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala	
165 170 175	
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Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser	
180 185 190	
atc ctg ttg gcg ccg gcc acc gca gag ctg gag ccc ttg gct gat gga	1522
Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly	
195 200 205 210	
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Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu	
215 220 225	
ctc tcg gtc tat ggg aaa ctc agg aag gtg gcc aag atg ggg ccc tac	1618
Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly Pro Tyr	
230 235 240	
agc atg ttc tgc aaa ctc ctc ggc atg tgg aga cac atc tgc acc ccg	1666
Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro	
245 250 255	
aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg	1714
Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met	
260 265 270	
aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac	1762
Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn	
275 280 285 290	
tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac	1810
Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn	
295 300 305	
aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag	1858
Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln	
310 315 320	
ctc gag agg gca gag cca cag tcc ctg gac ggc gtg gac tgaggccggt	1907
Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp	
325 330 335	
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gccaagggtta ggagccctac actaggagcc caggatggga cggcgcatca gccgagaggg	2027
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 Met Cys Trp Val Ile Asn His Ala Ile
 1 5
 ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat 159
 Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His
 10 15 20 25
 tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag 207
 Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln
 30 35 40
 ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc 255
 Leu Cys Leu Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe
 45 50 55
 agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc 303
 Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr
 60 65 70
 acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg 352
 Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg
 75 80 85
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 aaaaaaaaaa aaaaaa 428

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 atttggtctgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa 175
 Met Lys Ile Ala Leu Cys Gln
 1 5
 aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act 223
 Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr
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 gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act 271
 Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr
 25 30 35
 gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc 319
 Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu
 40 45 50 55
 tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt 367

Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys
60 65 70
aaa agc tgt gct tca aga aat cac aaa aac att ttc ctg cac cta cta 415
Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu
75 80 85
cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg 463
His Ser Leu Ser Ala Ala
90
caagaaatgc ttttttgtat gtgtcatgtc tgtttgtttt tcaattaaga gaggaaagca 523
ttaggcagat ggaatgtaca tgtgaggatg aggagacaga aaacaagtag ccctttccat 583
caagatagag ggttttctgg ggttgctggc tattgaatgt cactcctgat ttctctttcc 643
aaggcactgt accaccagcc tactgagatt gtgtgggagc tttcatgggg gttgtatttc 703
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aaaaaa 769

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Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys
1 5 10 15
ttt gcc aag ctc acc aac acc tac tgt ctg gta gcg atc gga ggc tca 155
Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser
20 25 30
gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc 203
Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro
35 40 45
gtg gtg cac gcg tct atc gcc ggc tgc cgc atc atc ggg cgc atg tgt 251
Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys
50 55 60
gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt 299
Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu
65 70 75
cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt 347
Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu
80 85 90 95
cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag 396
Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
100 105
gatgagctgt cctctcttct tcaagtcccc cttgtggcgg ggactgtgaa ccgaggcagt 456
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tgtacctgat gctggcaggg aggtggcaga gagctcactg ggactgaggg gctgggcacc 756
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tggactctct	tcagcttctg	gagacctcac	tatcctatt	atg tct ttg tgt gaa		474
				Met Ser Leu Cys Glu		
				1 5		
gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc						522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly						
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tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc						570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly						
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agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt						618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser						
	40		45		50	
acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca						666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser						
	55		60		65	
gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg						714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val						
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ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat						762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His						
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cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat						810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His						
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ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat						858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp						
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gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta						906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val						
	135		140		145	
cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg						954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met						
	150		155		160	165
gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt						1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu						
	170		175		180	
agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca						1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro						
	185		190		195	
tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac						1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn						
	200		205		210	

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Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly	
215 220 225	
gat gga gat ttt cag ttc aga cca ttt ttt gcg ggt tct ccc aca gca	1194
Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala	
230 235 240 245	
cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa	1242
Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu	
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Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile	
265 270 275	
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Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala	
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Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu	
30 35 40	
gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctc ttc cca	197
Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro	
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Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser	
60 65 70 75	
tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat	293
Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn	
80 85 90	
gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata	341
Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile	
95 100 105	
ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt	389
Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe	
110 115 120	
tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc	437
Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val	
125 130 135	
ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc	485
Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser	
140 145 150 155	
atg gca ctc att ata att gac tgg att tat gat cct cca aat tcc aag	533

Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys
160 165 170
cat cac taacacaagg aaaaatactt tctttttcta ttggaaatgg ttacaagtta 589
His His
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Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe
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aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct 150
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala
25 30 35
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa 198
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys
40 45 50 55
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga 246
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly
60 65 70
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc 294
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile
75 80 85
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg 342
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu
90 95 100
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat 390
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His
105 110 115
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Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr
120 125 130 135
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Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val
140 145 150
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att 534
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile
155 160 165
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Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp
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185 190 195

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220 225 230
ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga 774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg
235 240 245
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Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr
250 255 260
cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt 870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe
265 270 275
gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct 918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro
280 285 290 295
gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct 966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser
300 305 310
cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc 1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val
315 320 325
cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga 1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly
330 335 340
gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc 1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe
345 350 355
ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taaaaatatt acttcatggt 1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu
360 365 370
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Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr
20 25 30
ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att 146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile
35 40 45

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Tyr	Leu	Val	Ser	Leu	Pro	Phe	Val	Cys	Leu	Cys	Leu	Tyr	Phe	Ser	Leu	
	50						55					60				
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Tyr	Val	Met	Met	Ile	Tyr	Phe	Asp	Met	Glu	Val	Trp	Ala	Leu	Gly	Leu	
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His	Glu	Asn	Ser	Gly	Ser	Glu	Trp	Thr	Ser	Val	Leu	Leu	Tyr	Val	Pro	
	80				85					90					95	
agc	atc	atc	tat	gcc	att	gtg	att	gag	atc	atg	aat	cgt	ctc	tat	cga	338
Ser	Ile	Ile	Tyr	Ala	Ile	Val	Ile	Glu	Ile	Met	Asn	Arg	Leu	Tyr	Arg	
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tat	gct	gcc	gag	ttt	tta	act	tca	tgg	gag	aat	cac	aga	ttg	gaa	tct	386
Tyr	Ala	Ala	Glu	Phe	Leu	Thr	Ser	Trp	Glu	Asn	His	Arg	Leu	Glu	Ser	
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Ala	Tyr	Gln	Asn	His	Leu	Ile	Leu	Lys	Val	Leu	Val	Phe	Asn	Phe	Leu	
		130					135					140				
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Asn	Cys	Phe	Ala	Ser	Leu	Phe	Tyr	Ile	Ala	Phe	Val	Leu	Lys	Asp	Met	
	145					150					155					
aag	ctt	ttg	cgc	cag	agc	ttg	gcc	act	ctc	cta	att	acc	tcc	cag	atc	530
Lys	Leu	Leu	Arg	Gln	Ser	Leu	Ala	Thr	Leu	Leu	Ile	Thr	Ser	Gln	Ile	
	160				165					170					175	
ctc	aac	caa	att	atg	gaa	tct	ttt	ctt	cct	tat	tgg	ctc	caa	agg	aag	578
Leu	Asn	Gln	Ile	Met	Glu	Ser	Phe	Leu	Pro	Tyr	Trp	Leu	Gln	Arg	Lys	
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His	Gly	Val	Arg	Val	Lys	Arg	Lys	Val	Gln	Ala	Leu	Lys	Ala	Asp	Ile	
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gat	gct	aca	tta	tat	gaa	caa	gtc	atc	ctg	gaa	aaa	gaa	atg	gga	act	674
Asp	Ala	Thr	Leu	Tyr	Glu	Gln	Val	Ile	Leu	Glu	Lys	Glu	Met	Gly	Thr	
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Tyr	Leu	Gly	Thr	Phe	Asp	Asp	Tyr	Leu	Glu	Leu	Phe	Leu	Gln	Phe	Gly	
	225					230					235					
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Tyr	Val	Ser	Leu	Phe	Ser	Cys	Val	Tyr	Pro	Leu	Ala	Ala	Ala	Phe	Ala	
	240				245					250				255		
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Val	Leu	Asn	Asn	Phe	Thr	Glu	Val	Asn	Ser	Asp	Ala	Leu	Lys	Met	Cys	
				260					265					270		
agg	gtc	ttc	aaa	cgt	cca	ttc	tca	gaa	cct	tca	gcc	aat	att	ggg	gtg	866
Arg	Val	Phe	Lys	Arg	Pro	Phe	Ser	Glu	Pro	Ser	Ala	Asn	Ile	Gly	Val	
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Trp	Gln	Leu	Ala	Phe	Glu	Thr	Met	Ser	Val	Ile	Ser	Val	Val	Thr	Asn	
		290					295					300				
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Cys	Ala	Leu	Ile	Gly	Met	Ser	Pro	Gln	Val	Asn	Ala	Val	Phe	Pro	Glu	
	305					310					315					
tca	aaa	gca	gac	ctc	att	ttg	att	gta	gta	gca	gtg	gag	cac	gca	ctc	1010
Ser	Lys	Ala	Asp	Leu	Ile	Leu	Ile	Val	Val	Ala	Val	Glu	His	Ala	Leu	
	320				325					330				335		
ctg	gct	tta	aag	ttt	ata	ctt	gca	ttt	gcc	ata	cct	gat	aag	cca	cgg	1058
Leu	Ala	Leu	Lys	Phe	Ile	Leu	Ala	Phe	Ala	Ile	Pro	Asp	Lys	Pro	Arg	
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cat	atc	cag	atg	aaa	cta	gcc	aga	ctg	gaa	ttt	gag	tct	ttg	gag	gca	1106

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His Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala
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Leu Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu
      370      375      380
cca atg gaa agc ggg aag gag aag gca acc tgagtgccca gcgtgcccag      1204
Pro Met Glu Ser Gly Lys Glu Lys Ala Thr
      385      390
ctgcctctgtt ggcagaggcc tgtgtctgtg ccacacctgc caccgtggca ggggggggtac      1264
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Ala Val Glu Glu Leu Val Ser Gly Val Arg Gln Ala Ala Asp Phe Ala
      10      15      20
gag cag ttc cgc tcc tac tca gag agc gag aag caa tgg aag gcc cgc      148
Glu Gln Phe Arg Ser Tyr Ser Glu Ser Glu Lys Gln Trp Lys Ala Arg
      25      30      35      40
atg gaa ttc atc ctg cgc cac ctg ccc gac tac cgc gac ccg ccc gac      196
Met Glu Phe Ile Leu Arg His Leu Pro Asp Tyr Arg Asp Pro Pro Asp
      45      50      55
ggc agt ggc cgc ctg gac cag ctg ctc tcc ctc tcc atg gtc tgg gcc      244
Gly Ser Gly Arg Leu Asp Gln Leu Leu Ser Leu Ser Met Val Trp Ala
      60      65      70
aac cat ctc ttc cta ggc tgc agt tac aat aaa gac ctt tta gac aag      292
Asn His Leu Phe Leu Gly Cys Ser Tyr Asn Lys Asp Leu Leu Asp Lys
      75      80      85
gtg atg gaa atg gcc gat ggg att gaa gtg gaa gac ctg cca caa ttt      340
Val Met Glu Met Ala Asp Gly Ile Glu Val Glu Asp Leu Pro Gln Phe
      90      95      100
act acc aga agt gaa tta atg aaa aag cat caa agc taagccagaa      386
Thr Thr Arg Ser Glu Leu Met Lys Lys His Gln Ser
      105      110      115
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atagaccaca gcagctctct taagactcct ggtattacca acataaagag gcaggtggaa      506
tgagaaggac tctgtctaga ttggcttttt taacattctc attttcccag gagttatcac      566
tgtaaaagta tgcattgata tttatgtatt tataaatcat gcactctaag atgagttcat      626
caacattgta aaagccctct tttctgtttt cagggttttt tttttcttat cgacaaggtc      686

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gaattttttgt	ttaaaatgcc	tttttgggct	gggccacagt	ggccttatgc	ccataataat	926
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tgggaggtgg	aggttgcagt	gagccaagat	cgcaccattg	cactccatcc	tgggcgacaa	1166
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		1 5 10				
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag						158
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu						
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Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala						
	30	35	40			
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt						254
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly						
	45	50	55			
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Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys						
	60	65	70	75		
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag						350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln						
	80	85	90			
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc						398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro						
	95	100	105			
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Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg						
	110	115	120			
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc						494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro						
	125	130	135			
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga						542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg						
	140	145	150	155		
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgtttctccg						596
Arg Arg Ala Arg Asp Thr Arg Ser						
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ccatcaaggt ttgagtcac aaaagtggac ctccctatca tgcttccct tccctctagc						716
atgtgggaag ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt						776

gctaaataag ggcttcctct gccttctacc tacagtgcac ttgaactgcc ttctgaaaga 836
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 Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val
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 Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu
 30 35 40
 gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat 195
 Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn
 45 50 55 60
 ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg 243
 Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala
 65 70 75
 aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg 291
 Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu
 80 85 90
 ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca 339
 Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala
 95 100 105
 tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag ctt 387
 Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu
 110 115 120
 ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt 435
 Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys
 125 130 135 140
 gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc 483
 Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro
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 Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His
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 acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg 579
 Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr
 175 180 185
 ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag 627
 Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln
 190 195 200
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 Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu
 205 210 215 220
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 Glu Thr Leu Glu Lys Thr Ile His Glu Glu
 225 230

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aagtaactgt gaacaaataa tttgttctgt gccttttgcc tggtatatag caaatactca	845
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	Met Glu Arg Pro
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gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa	162
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu	
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agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta	210
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Phe Phe Thr Ala Leu	
25 30 35	
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Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile	
40 45 50	
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct	306
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala	
55 60 65	
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Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val	
70 75 80	
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Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln	
85 90 95 100	
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat	455
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 <213> Homo sapiens

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 <221> CDS
 <222> 72..350

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tgcaggcggc c atg gat tcc ttg cgg aaa atg ctg atc tca gtc gca atg	110
	Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met
	1 5 10
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc	158
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr	

15	20	25	
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag			206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln			
30	35	40	45
gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg			254
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu			
50	55	60	
gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg			302
Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg			
65	70	75	
aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc ggc ggg agg tca ccg			350
Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro			
80	85	90	
tgagaccgga cttgcctccg tgggcgcgag accttggtt gggcgcagga atccgaggca			410
gcctttctcc ttcgtgggccc cagcggagag tccggaccga gataccatgc caggactctc			470
cggggtcctg tgagctgccc tcgggtgagc acgtttcccc caaaccttg actgactgct			530
ttaaggtccc caaggcgggc cagggccgag acgcgagtcg gatgtggtga actgaaagaa			590
ccaataaaat catgttcctc cacccaaaaa aaaaaaaaaa aa			632
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	Met Gly His Gly Asp Glu		
	1	5	
atc gtt ctt gcg gac ttg aac ttc ccg gcc tcc tcc atc tgc cag tgt			103
Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys			
10	15	20	
ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg			151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu			
25	30	35	
gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg			199
Glu Ala Val Leu Lys Leu Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro			
40	45	50	
gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag			247
Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln			
55	60	65	70
acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt			295
Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys			
75	80	85	
gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct			343
Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala			
90	95	100	
aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga			391
Lys Lys Ala Phe Ala Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly			
105	110	115	
aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg			436
Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu			
120	125	130	
taggcctggt gaagaccacc tgggcgggaa gaggaactgg gggcacctg agctccagta			496
ccaccactca caacaggcct ccagtgga gctccagac ctgggacctg gccagggtc			556

Ser	Arg	Tyr	Asn	Phe	Arg	Arg	Thr	Phe	Gly	Ile	Glu	Leu	Ser	Ser	Asn		
				15					20					25			
tct	tcc	tat	tgc	aaa	cga	gga	aat	ggc	tac	aga	agc	aga	gtg	ccc	aaa		327
Ser	Ser	Tyr	Cys	Lys	Arg	Gly	Asn	Gly	Tyr	Arg	Ser	Arg	Val	Pro	Lys		
			30					35					40				
gaa	tgc	gaa	tgc	aac	tgg	ctt	cat	ctt	gaa	agc	gac	act	ctg	aag	aaa		375
Glu	Cys	Glu	Cys	Asn	Trp	Leu	His	Leu	Glu	Ser	Asp	Thr	Leu	Lys	Lys		
			45				50					55					
tta	ccc	ata	att	tct	ccc	tct	tgg	aca	tgc	aga	att	atc	ctg	ttc	ttg		423
Leu	Pro	Ile	Ile	Ser	Pro	Ser	Trp	Thr	Cys	Arg	Ile	Ile	Leu	Phe	Leu		
	60					65				70							
tat	ttt	tct	ggc	cag	ctt	ctc	caa	ctt	tcc	ctt	tct	tgt	ttg	caa	cta		471
Tyr	Phe	Ser	Gly	Gln	Leu	Leu	Gln	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu		
	75			80					85				90				
att	aaa	ctt	taaggataaaa	aaaaaaaaaaaa	aa												502
Ile	Lys	Leu															
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<222> 171...1670																	
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gccattcct	tgaaaactaa	aagggtccctg	actcccagtc	tgccagccatc	ctgggcctgc												120
tgagctctga	ttcaagtgcc	tgccctctgcc	ccttggtggg	ctgaagcttc	atg gag												176
					Met Glu												
					1												
gta	tcc	acc	aac	ccc	tcc	tcc	aac	atc	gat	cca	ggc	aac	tat	gtt	gaa		224
Val	Ser	Thr	Asn	Pro	Ser	Ser	Asn	Ile	Asp	Pro	Gly	Asn	Tyr	Val	Glu		
		5					10					15					
atg	aat	gat	tca	atc	acc	cac	cta	ccc	tct	aaa	gtg	gtg	ata	caa	gat		272
Met	Asn	Asp	Ser	Ile	Thr	His	Leu	Pro	Ser	Lys	Val	Val	Ile	Gln	Asp		
	20					25				30							
att	act	atg	gag	cta	cac	tgc	cct	ctg	tgc	aat	gat	tgg	ttc	cga	gac		320
Ile	Thr	Met	Glu	Leu	His	Cys	Pro	Leu	Cys	Asn	Asp	Trp	Phe	Arg	Asp		
	35				40					45				50			
cca	ctg	atg	cta	agc	tgt	ggc	cac	aac	ttc	tgt	gaa	gcc	tgt	atc	caa		368
Pro	Leu	Met	Leu	Ser	Cys	Gly	His	Asn	Phe	Cys	Glu	Ala	Cys	Ile	Gln		
				55				60					65				
gac	ttt	tgg	agg	ctg	caa	gca	aag	gaa	aca	ttc	tgt	cct	gag	tgt	aag		416
Asp	Phe	Trp	Arg	Leu	Gln	Ala	Lys	Glu	Thr	Phe	Cys	Pro	Glu	Cys	Lys		
		70					75					80					
atg	cta	tgt	cag	tat	aac	aac	tgt	aca	ttc	aac	cct	gta	ctg	gac	aag		464
Met	Leu	Cys	Gln	Tyr	Asn	Asn	Cys	Thr	Phe	Asn	Pro	Val	Leu	Asp	Lys		
	85				90					95							
ttg	gta	gag	aag	att	aag	aag	tta	ccc	tta	ctc	aag	ggc	cat	cca	cag		512
Leu	Val	Glu	Lys	Ile	Lys	Lys	Leu	Pro	Leu	Leu	Lys	Gly	His	Pro	Gln		
	100					105					110						
tgc	cca	gag	cat	gga	gag	aac	ctg	aaa	ctg	ttc	agt	aaa	cca	gat	ggg		560
Cys	Pro	Glu	His	Gly	Glu	Asn	Leu	Lys	Leu	Phe	Ser	Lys	Pro	Asp	Gly		
	115				120				125						130		
aaa	ctg	atc	tgc	ttt	caa	tgc	aag	gat	gct	cgg	ttg	tct	gtg	ggg	cag		608
Lys	Leu	Ile	Cys	Phe	Gln	Cys	Lys	Asp	Ala	Arg	Leu	Ser	Val	Gly	Gln		

tct aag gag ttc	135	caa atc tct	140	gat gct gtc	cat ttc ttc	145	atg gag	656
Ser Lys Glu Phe	Leu Gln Ile	Ser Asp Ala	Val His Phe	Phe Met Glu				
	150		155		160			
gag ctt gcc atc	caa cag ggt	caa ctg gag	aca act ctg	aag gag ctt				704
Glu Leu Ala Ile	Gln Gln Gly	Gln Leu Glu	Thr Thr Leu	Lys Glu Leu				
	165		170		175			
cag acc ctg agg	aac atg cag	aag gaa gct	att gct gct	cac aag gaa				752
Gln Thr Leu Arg	Asn Met Gln	Lys Glu Ala	Ile Ala Ala	His Lys Glu				
	180		185		190			
aac aag cta cat	ctg cag caa	cat gtg tcc	atg gag ttt	cta aag ctg				800
Asn Lys Leu His	Leu Gln Gln	His Val Ser	Met Glu Phe	Leu Lys Leu				
	195		200		205		210	
cat cag ttc ctg	cac agc aaa	gaa aag gac	att tta act	gag ctc cgg				848
His Gln Phe Leu	His Ser Lys	Glu Lys Asp	Ile Leu Thr	Glu Leu Arg				
	215		220		225			
gaa gag ggg aaa	gcc ttg aat	gag gag atg	gag ttg aat	ctg agc cag				896
Glu Glu Gly Lys	Ala Leu Asn	Glu Glu Met	Glu Leu Asn	Leu Ser Gln				
	230		235		240			
ctt cag gag caa	tgt ctc tta	gcc aag gat	atg ttg gtg	agc att cag				944
Leu Gln Glu Gln	Cys Leu Leu	Ala Lys Asp	Met Leu Val	Ser Ile Gln				
	245		250		255			
gca aag acg gaa	caa cag aac	tcc ttc gac	ttt ctc aaa	gac atc aca				992
Ala Lys Thr Glu	Gln Gln Asn	Ser Phe Asp	Phe Leu Lys	Asp Ile Thr				
	260		265		270			
act ctc tta cat	agc ttg gag	caa gga atg	aag gtg ctg	gca acc aga				1040
Thr Leu Leu His	Ser Leu Glu	Gln Gly Met	Lys Val Leu	Ala Thr Arg				
	275		280		285		290	
gag ctt att tcc	aga aag ctg	aac ctg ggc	cag tac aaa	ggc cct atc				1088
Glu Leu Ile Ser	Arg Lys Leu	Asn Leu Gly	Gln Tyr Lys	Gly Pro Ile				
	295		300		305			
cag tac atg gta	tgg agg gaa	atg cag gac	act ctc tgc	cca ggc ctg				1136
Gln Tyr Met Val	Trp Arg Glu	Met Gln Asp	Thr Leu Cys	Pro Gly Leu				
	310		315		320			
tct cca cta act	ctg gac cct	aaa aca gct	cac cca aat	ctg gtg ctc				1184
Ser Pro Leu Thr	Leu Asp Pro	Lys Thr Ala	His Pro Asn	Leu Val Leu				
	325		330		335			
tcc aaa agc caa	acc agc gtc	tgg cat ggt	gac att aag	aag ata atg				1232
Ser Lys Ser Gln	Thr Ser Val	Trp His Gly	Asp Ile Lys	Lys Ile Met				
	340		345		350			
cct gat gat cct	gag agg ttt	gac tca agt	gtg gct gta	ctg ggc tca				1280
Pro Asp Asp Pro	Glu Arg Phe	Asp Ser Ser	Val Ala Val	Leu Gly Ser				
	355		360		365		370	
aga ggc ttc acc	tct gga aag	tgg tac tgg	gaa gta gaa	gta gca aag				1328
Arg Gly Phe Thr	Ser Gly Lys	Trp Tyr Trp	Glu Val Glu	Val Ala Lys				
	375		380		385			
aag aca aaa tgg	aca gtt gga	gtt gtc aga	gaa tcc atc	att cgg aag				1376
Lys Thr Lys Trp	Thr Val Gly	Val Val Arg	Glu Ser Ile	Ile Arg Lys				
	390		395		400			
ggc agc tgt cct	cta act cct	gag caa gga	ttc tgg ctt	tta aga cta				1424
Gly Ser Cys Pro	Leu Thr Pro	Glu Gln Gly	Phe Trp Leu	Leu Arg Leu				
	405		410		415			
agg aac caa act	gat cta aag	gct ctg gat	ttg cct tct	ttc agt ctg				1472
Arg Asn Gln Thr	Asp Leu Lys	Ala Leu Asp	Leu Pro Ser	Phe Ser Leu				
	420		425		430			
aca ctg act aac	aac ctc gac	aag gtg ggc	ata tac ctg	gat tat gaa				1520
Thr Leu Thr Asn	Asn Leu Asp	Lys Val Gly	Ile Tyr Leu	Asp Tyr Glu				
	435		440		445		450	

gga gga cag ttg tcc ttc tac aat gct aaa acc atg act cac att tac 1568
 Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His Ile Tyr
 455 460 465
 acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc 1616
 Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
 470 475 480
 tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat 1664
 Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
 485 490 495
 cca cag taatgagtca taatattata caaattcaga gtgttattaa agagggttttg 1720
 Pro Gln
 500
 aaataaaaaa aaaaaaaaaa 1739

<210> 226
 <211> 657
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 199..618

<400> 226
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 ctacctaatg ctttctcaga taaataagca tgaagaaaag tcaaagtcca ttctagctct 120
 aaaataagga atgaaatgtt ttctgatgat gattttttgt tttcatctga taataatttt 180
 atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc 231
 Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
 1 5 10
 agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg 279
 Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
 15 20 25
 ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac 327
 Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
 30 35 40
 tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag 375
 Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
 45 50 55
 gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct 423
 Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
 60 65 70 75
 cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa 471
 Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
 80 85 90
 cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac 519
 His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
 95 100 105
 cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc 567
 Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
 110 115 120
 cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata 615
 Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
 125 130 135
 tgc tagtactaat aaaaccaaca tgttaaaaaa aaaaaaaaaa 657
 Cys
 140

<210> 227
 <211> 888
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 182..481

<400> 227
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 aagctgctga tcattcagttt caggaagtca gcatggatca gccttacgtt catggcctcc 120
 aggccttatt ctctgcctc acagggaccg gccaggatct ctatccttac agcacgttgg 180
 a atg tat atg ctc ctc tcc cca cat cgc ctt agg gag cag gca ggt gtc 229
 Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
 1 5 10 15
 agg ggc agc ata agg acg gcc aac agg aca gaa gac ggg ttg aag atc 277
 Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
 20 25 30
 cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc 325
 Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
 35 40 45
 ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga 373
 Leu His Ser Ala Ser Leu Gln Ala Pro Gly Gly Ile Leu Met Gly
 50 55 60
 cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca 421
 Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
 65 70 75 80
 tct gca cct cct ctc aga gaa agc ctg atg cct act aaa gga ctt ggg 469
 Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
 85 90 95
 tgg tgg acg cag tgaccctcag tctggagctt gttcactgaa cattggagac 521
 Trp Trp Thr Gln
 100
 tatcatttgc gcagatgggc ttgggcctct atgagcagca ggctgcaccc cacagtgacc 581
 tctcattct actctgaggg atcttcatga aagcagatgt ccattgaaaa gcacccaagt 641
 gcagtctcag ctgatgaact tcagaggcga ttgagacaaa ggctctcggt cccctctgcc 701
 cttggatggg gcctctggta tgcacttggc ctctgtgtct ttatttagac tggtcacttc 761
 acaaccctc atgtcacccc acccctaacc gtgcccactc tgggtcctcc cctcaactgc 821
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 aaaaaaa 888

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 <213> Homo sapiens

<220>
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 <222> 161..517

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 cctccctcog cccgcgcctc tccttagtcc ttgagatgag atg gca agt tac agc 175
 Met Ala Ser Tyr Ser
 1 5
 ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc 223


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tgg aat gca ggc atc atg acg gtg atg tca gct ctg tcg gtg gcc ccc 448
Trp Asn Ala Gly Ile Met Thr Val Met Ser Ala Leu Ser Val Ala Pro
      110      115      120
tcc aag gcc cgc gag tac tcc aag gag ggc tgg gag tat gtg aag gcg 496
Ser Lys Ala Arg Glu Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala
      125      130      135
cgc acc aag tagcgagtca gcagggggccg cctgcccccg ccagaacggg 545
Arg Thr Lys
      140
cagggctgcc actgacctga agactccgga ctgggacccc actccgaggg cagctccccg 605
ccttgccggc ccaataaagg acttcagaag tcaaaaaaaaa aaaaaaaaaa 654

<210> 230
<211> 635
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<213> Homo sapiens

<220>
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<222> 56..382

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                                     1
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Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
      5      10      15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca 154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
      20      25      30
ttt caa cag att cgg tgc tat tct gca cct gtt gct gct gag ccc ttt 202
Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro Phe
      35      40      45
ctc agt ggg act agt tcg aac tat gtg gag gag atg tac tgt gct tgg 250
Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala Trp
      50      55      60      65
ctg gaa aac ccc aaa agt gta cat aag aca ggg tcc cac tgt tgt cca 298
Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys Pro
      70      75      80
ggc tgg agt gca gtg gcg gga tct cgg ctt gct gca acc tcc gac tcc 346
Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp Ser
      85      90      95
tgg gtt caa gtg att ctt atg cct cag cct ccc gag taactgggac 392
Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu
      100      105
tacagggtgca cgtcaccacg cctgactagt ttttgtatatt ttagtagaga tgggatttta 452
ctttgtttggc caggctggtc ttgaaccctt ggctcgaagt gatccacca ccttggcctc 512
ccaaagtgcg gggattacag gtatgatcaa ccacgcctgg ccatgtcatg ccttgtgaca 572
gaattccttt attctgtttt gagccaataa atatttatag gtttcgaaaa aaaaaaaaaa 632
aaa 635

<210> 231
<211> 634
<212> DNA
<213> Homo sapiens

<220>

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<221> CDS
<222> 56..355

<400> 231

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Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
          5          10          15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca      154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
          20          25          30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc      202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro Phe
          35          40          45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc      250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
50          55          60          65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag      298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
          70          75          80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct      346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
          85          90          95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca      395
Gly Phe Lys
          100
ggtgcacgctc accacgcctg actagttttt gtatttttag tagagatggg attttacttt      455
gttggccagg ctggtcttga acccctggcc tcaagtgatc caccacctt ggccctccaa      515
agtgtcggga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat      575
tcctttattc tgttttgagc caataaatat ttataggttt cgaaaaaaaa aaaaaaaaaa      634

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<210> 232

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..498

<400> 232

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          Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
          1          5          10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att      159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
          15          20          25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat      207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
          30          35          40
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg      255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45          50          55          60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc      303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile

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aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc		234
	Met Ala Thr His Pro Asp Gly Phe	
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Arg Leu Glu Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr		
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Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg		
25 30 35 40		
aat tcc aac acc atg tcg gcg gct gcc ctg gct gcc ccc agc ctg ggc		378
Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly		
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Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp		
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atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc		474
Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys		
75 80 85		
cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc		522
Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly		
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gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg		570
Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu		
105 110 115 120		
gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc		612
Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys		
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Gly	Gly	Glu	Pro	Arg	Thr	Gly	Ala	Pro	Ala	Asn	Ser	Pro	Ser	Cys	Pro
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cag	gag	atg	cca	ctg	cag	gac	cca	agg	agc	agg	gag	gag	gcg	gcc	agg
Gln	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg
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Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln
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Leu	Val	Ser	Ser	Leu	Phe	Phe	His	Val	Pro	Ala	Gly	Leu	Leu	Ala	Leu
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Phe	Thr	Leu	Arg	His	His	Lys	Tyr	Gly	Arg	Phe	Met	Ser	Val	Ser	Ile
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Phe	Glu	Ala	Leu	Thr	Leu	Gly	Thr	Gly	Gln	Thr	Phe	Cys	Val	Leu	Val
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gtc	tcc	ttt	tta	cgg	att	tta	gct	act	cta	tagcatacat	ccttatgctg				
Val	Ser	Phe	Leu	Arg	Ile	Leu	Ala	Thr	Leu						
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acc tcc ttc ccc agg cag cca ttg tta aca ttt ttt gaa tat cta gaa	151								
Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe Phe Glu Tyr Leu Glu									
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aaa gtc ctt tgt tca gga tta ttt tcc cac tct gcc aag agt cac cat	199								
Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser Ala Lys Ser His His									
	40		45		50				
gac ctg ctc aca cgc cac cct tat gaa act gcc gcg cca ctt ctc agc	247								
Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala Ala Pro Leu Leu Ser									
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tcc cat ttg att ctc aca gaa gct cta cga aat ggg ttg ggc aaa tgt	295								
Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn Gly Leu Gly Lys Cys									
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cat gat cct cat ttc aca ggg gaa gaa act gag gcc cag agg ggg aaa	343								
His Asp Pro His Phe Thr Gly Glu Glu Thr Glu Ala Gln Arg Gly Lys									
	90		95		100				
ctg act acc taaaattgcc atgtaggccg gcgcgggtggc tcacgcctgt	392								
Leu Thr Thr									
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cctggctggc acttgaagcc ccgtctctac tagggatata aataattggc cgggtgtggt	512								
ggcgggcgcc tgtgkwccca gctgttcggc aggctgagga gggcgaatgg tgtgagcctg	572								
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Leu Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln	
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Arg Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr	
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Asn Glu Ala Gln Met Ala Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln	
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Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn	
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Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro	
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Glu Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser	
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115 120 125	
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Ala Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile	
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Leu Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile	
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Tyr Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr	
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Ile Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys	
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Tyr Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn	
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tgc ctg gaa ggg acc cac gag ttt ttt gag gcc att ggg ttc cag aag	671
Cys Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln Lys	
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Val Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val	
225 230 235	
ctg agc gag acc acc ttg gcc cag ccc cag agc ctg gag agg cac aag	767
Leu Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys	
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gaa cag ctg ctg gct gcg gag ccc gtg cgc gcc aag ctg gac agg cag	815
Glu Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg Gln	
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cgc cgc gtc ttc cag ccc tcg ccc ctg gcc tcg cag ttc gaa ctg cct	863
Arg Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu Pro	
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Gly Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln Arg	

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Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr			
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Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe			
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Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala			
355	360	365	
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Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp			
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Leu Ser Ala Ile Glu Lys Leu Leu			
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Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala	
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Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly	
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Thr Val Lys Arg Tyr Val Arg Lys Gly Val Pro Leu Glu His Arg Ala	
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Pro Gly Tyr Tyr His Gln Leu Leu Gln Gly Glu Arg Asn Pro Arg Leu	
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Glu Asp Ala Ile Arg Thr Asp Leu Asn Arg Thr Phe Pro Asp Asn Val	
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Lys Phe Arg Lys Thr Thr Asp Pro Cys Leu Gln Arg Thr Leu Tyr Asn	
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ctgctgtgtg tggtgccaga agtgtggctt cccgaggccc ggccctcccca ctgggtcctg	1310
gacctggcgc aggcctgata gactcaggtc ctgatgaggc cgttgtggga gctgtacctg	1370
acagcccttc tgaggaagcc aagacgccag gagaggctca ggccctgggag tcagtagttt	1430
cctaagaggg agtggaggct cggggccact ctgggtgcag catggcaaac gtgggcggtg	1490
tttcagcagc tgggccttca tcaaagagaa gaccatgttg gccgggcgcg gtggctcacg	1550
cctgcagtc cagcactttg ggaggccaag gcgtgtggat cacctgaggt caggagttca	1610
agaccagcct ggccaacacg gtgaaacccc gtctctacta aaaaatacaa aaattagcca	1670
ggtgtggtgg ctacacgtta ttagtccca gttactcggg aggctgaggc acgagaatca	1730
cttgaacctg ggaggcggag gttgcagtga gccgagatcg cgccactgca ctccagcctg	1790
ggcaacagag tgagactctg tctcaaaaaa aaaaaaaaaa a	1831

<210> 241
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..608

<400> 241	
aaggacttaa gcgccccgga gccggggaggc gaacttgga cccgctggcc tcgctcgggtg	60
cgcgcctccc tccccgc atg cag ccc gcc gag cgc tcg cgg gtc ccc agg	110
Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg	
1 5 10	
atc gac ccg tac gga ttc gag cgg cct gag gac ttc gac gac gcc gcc	158
Ile Asp Pro Tyr Gly Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala	
15 20 25	
tac gag aag ttt ttc tcc agc tac ctg gtc acg ctc acc cgc agg gcg	206
Tyr Glu Lys Phe Phe Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala	
30 35 40	
atc aaa tgg tcc cgg ctg ctg cag ggc ggg ggc gtc ccc agg agc cgg	254
Ile Lys Trp Ser Arg Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg	
45 50 55	
aca gtg aag cgc tat gtc cgg aaa ggg gtc ccg ctg gag cac cgt gcc	302

Thr	Val	Lys	Arg	Tyr	Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala		
60					65				70						75		
cgc	gtc	tgg	atg	gtg	ctg	agt	ggg	gcc	cag	gcg	cag	atg	gac	cag	aat		350
Arg	Val	Trp	Met	Val	Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn		
				80				85						90			
ccc	ggc	tac	tac	cac	cag	ctt	ctc	cag	gga	gag	aga	aac	ccc	agg	ctg		398
Pro	Gly	Tyr	Tyr	His	Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu		
				95				100					105				
gag	gac	gcc	atc	agg	aca	gac	ctg	aac	cgg	acc	ttc	ccc	gac	aac	gtg		446
Glu	Asp	Ala	Ile	Arg	Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val		
		110					115					120					
aag	ttc	cgg	aag	acc	acg	gac	ccc	tgc	tta	cag	agg	acc	ctg	tac	aat		494
Lys	Phe	Arg	Lys	Thr	Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn		
		125				130					135						
gtg	ctg	ctg	gca	tat	ggg	cac	cat	aac	cag	gga	gtg	ggc	tac	tgc	cag		542
Val	Leu	Leu	Ala	Tyr	Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln		
				140		145			150					155			
gga	atg	aat	ttt	ata	gca	gga	tat	ctg	att	ctt	ata	aca	aat	aat	gat		590
Gly	Met	Asn	Phe	Ile	Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp		
				160				165					170				
aag	aat	ctt	ttt	ggc	tgt	tagatgctct	tggttgaaga	atactaccag									638
Lys	Asn	Leu	Phe	Gly	Cys												
				175													
attactacag	cccggccatg	ctgggcctga	agaccgacca	ggaggtcctc	ggggagctgg												698
tgcgggagaa	gctgccggct	gtggggggccc	tgatggagcg	tctcgggtgtg	ctgtggacgc												758
tgctgggtgtc	ccgctgggttc	atctgcctgt	ttgtggacat	cttgcccgtg	gagacagtgc												818
ttcggatctg	ggactgtttg	tttaacgaag	gctcgaagat	tatcttccgg	ttggccctga												878
ccttaattaa	gcagcaccag	gagttgattt	tggaagccac	cagcgttcca	gacatttgcg												938
ataagtttaa	gcagataacc	aaagggagtt	tcgtgatgga	gtgtcacacg	tttatgcagg												998
tgtgtggggc	tgacagtggc	tcagtcacct	cccagggggc	cccgccctcac	ctgcagcccg												1058
ggggctgctc	tgaccacccg	gaggatgcac	aggatgggca	ccagtgggca	tagggcacag												1118
gatgagcctc	cagctctgtc	ctgcatctgc	cccctgcgcc	tggcctccga	gggctttcct												1178
gtctatggcg	gcctgtgctt	cttgcccttg	gcactgcgga	cgctgctcct	ggtcctaattg												1238
gctgtactca	tctgtgtgtg	gtgggtgccag	aagtgtggct	tcccagggcc	cggcctcccc												1298
actgggtcct	ggacctggcg	caggccgtat	agactcaggt	cctgatgagg	gcgttggtggg												1358
agctgtacct	gacaggcctt	ctgaggaagc	caagacgcca	ggagaggctc	aggcctggga												1418
gtcagtagtt	tcctaagagg	gagtggaggc	tcggggccac	tctgggtgca	gcatggcaaa												1478
cgtgggcggt	atttcagcag	ctgggccttc	atcaaagaga	agaccatgtt	ggccggggcgc												1538
ggtggctcac	gcctgcagtc	ccagcacttt	gggaggccaa	ggcgtgtgga	tcacctgagg												1598
tcaggagttc	aagaccagcc	tggccaacac	ggtgaaaccc	cgtctctact	aaaaaataca												1658
aaaatttagcc	aggtgtgggtg	gctcacgctt	atgtagtccc	agttactcgg	gaggctgagg												1718
cacgagaatc	acttgaacct	gggaggcgga	ggttgacgtg	agccgagatc	gcgccactgc												1778
actccagcct	gggcaacaga	gtgagactct	gtctcaaaaa	aaaaaaaaaa	aa												1830

<210> 242

<211> 508

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -27...-1

<400> 242

Met	Asp	Pro	Lys	Leu	Gly	Arg	Met	Ala	Ala	Ser	Leu	Leu	Ala	Val	Leu		
	-25						-20						-15				
Leu	Leu	Leu	Leu	Leu	Glu	Arg	Gly	Met	Phe	Ser	Ser	Pro	Ser	Pro	Pro		
	-10					-5				1					5		

Pro	Ala	Leu	Leu	Glu	Lys	Val	Phe	Gln	Tyr	Ile	Asp	Leu	His	Gln	Asp
				10					15					20	
Glu	Phe	Val	Gln	Thr	Leu	Lys	Glu	Trp	Val	Ala	Ile	Glu	Ser	Asp	Ser
			25					30					35		
Val	Gln	Pro	Val	Pro	Arg	Phe	Arg	Gln	Glu	Leu	Phe	Arg	Met	Met	Ala
		40				45					50				
Val	Ala	Ala	Asp	Thr	Leu	Gln	Arg	Leu	Gly	Ala	Arg	Val	Ala	Ser	Val
	55				60					65					
Asp	Met	Gly	Pro	Gln	Gln	Leu	Pro	Asp	Gly	Gln	Ser	Leu	Pro	Ile	Pro
70					75					80				85	
Pro	Val	Ile	Leu	Ala	Glu	Leu	Gly	Ser	Asp	Pro	Thr	Lys	Gly	Thr	Val
				90					95					100	
Cys	Phe	Tyr	Gly	His	Leu	Asp	Val	Gln	Pro	Ala	Asp	Arg	Gly	Asp	Gly
			105					110					115		
Trp	Leu	Thr	Asp	Pro	Tyr	Val	Leu	Thr	Glu	Val	Asp	Gly	Lys	Leu	Tyr
		120				125						130			
Gly	Arg	Gly	Ala	Thr	Asp	Asn	Lys	Gly	Pro	Val	Leu	Ala	Trp	Ile	Asn
		135				140					145				
Ala	Val	Ser	Ala	Phe	Arg	Ala	Leu	Glu	Gln	Asp	Leu	Pro	Val	Asn	Ile
150					155					160				165	
Lys	Phe	Ile	Ile	Glu	Gly	Met	Glu	Glu	Ala	Gly	Ser	Val	Ala	Leu	Glu
				170					175					180	
Glu	Leu	Val	Glu	Lys	Glu	Lys	Asp	Arg	Phe	Phe	Ser	Gly	Val	Asp	Tyr
			185					190					195		
Ile	Val	Ile	Ser	Asp	Asn	Leu	Trp	Ile	Ser	Gln	Arg	Lys	Pro	Ala	Ile
		200				205						210			
Thr	Tyr	Gly	Thr	Arg	Gly	Asn	Ser	Tyr	Phe	Met	Val	Glu	Val	Lys	Cys
	215					220					225				
Arg	Asp	Gln	Asp	Phe	His	Ser	Gly	Thr	Phe	Gly	Gly	Ile	Leu	His	Glu
230				235						240				245	
Pro	Met	Ala	Asp	Leu	Val	Ala	Leu	Leu	Gly	Ser	Leu	Val	Asp	Ser	Ser
				250					255					260	
Gly	His	Ile	Leu	Val	Pro	Gly	Ile	Tyr	Asp	Glu	Val	Val	Pro	Leu	Thr
			265					270					275		
Glu	Glu	Glu	Ile	Asn	Thr	Tyr	Lys	Ala	Ile	His	Leu	Asp	Leu	Glu	Glu
		280					285					290			
Tyr	Arg	Asn	Ser	Ser	Arg	Val	Glu	Lys	Phe	Leu	Phe	Asp	Thr	Lys	Glu
	295					300					305				
Glu	Ile	Leu	Met	His	Leu	Trp	Arg	Tyr	Pro	Ser	Leu	Ser	Ile	His	Gly
310					315					320				325	
Ile	Glu	Gly	Ala	Phe	Asp	Glu	Pro	Gly	Thr	Lys	Thr	Val	Ile	Pro	Gly
				330					335					340	
Arg	Val	Ile	Gly	Lys	Phe	Ser	Ile	Arg	Leu	Val	Pro	His	Met	Asn	Val
			345					350					355		
Ser	Ala	Val	Glu	Lys	Gln	Val	Thr	Arg	His	Leu	Glu	Asp	Val	Phe	Ser
		360					365					370			
Lys	Arg	Asn	Ser	Ser	Asn	Lys	Met	Val	Val	Ser	Met	Thr	Leu	Gly	Leu
	375					380					385				
His	Pro	Trp	Ile	Ala	Asn	Ile	Asp	Asp	Thr	Gln	Tyr	Leu	Ala	Ala	Lys
390					395					400				405	
Arg	Ala	Ile	Arg	Thr	Val	Phe	Gly	Thr	Glu	Pro	Asp	Met	Ile	Arg	Asp
				410					415					420	
Gly	Ser	Thr	Ile	Pro	Ile	Ala	Lys	Met	Phe	Gln	Glu	Ile	Val	His	Lys
			425					430					435		
Ser	Val	Val	Leu	Ile	Pro	Leu	Gly	Ala	Val	Asp	Asp	Gly	Glu	His	Ser
		440					445					450			
Gln	Asn	Glu	Lys	Ile	Asn	Arg	Trp	Asn	Tyr	Ile	Glu	Gly	Thr	Lys	Leu
	455					460					465				

Phe Ala Ala Phe Phe Leu Glu Met Ala Gln Leu His
 470 475 480

<210> 243
 <211> 331
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 243
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn
 35 40 45
 Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val
 50 55 60 65
 Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His
 70 75 80
 Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp
 85 90 95
 Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg
 100 105 110
 Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Met Glu Ala
 115 120 125
 Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys
 130 135 140 145
 Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu
 150 155 160
 Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu
 165 170 175
 Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu
 180 185 190
 Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg
 195 200 205
 Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu
 210 215 220 225
 Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser
 230 235 240
 Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys
 245 250 255
 Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe
 260 265 270
 Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr
 275 280 285
 Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 290 295 300

<210> 244
 <211> 274

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17...-1

<400> 244
Met Asp Arg Pro Gly Phe Val Ala Ala Leu Val Ala Gly Gly Val Ala
-15 -10 -5
Gly Val Ser Val Asp Leu Ile Leu Phe Pro Leu Asp Thr Ile Lys Thr
1 5 10 15
Arg Leu Gln Ser Pro Gln Gly Phe Ser Lys Ala Gly Gly Phe His Gly
20 25 30
Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Ala
35 40 45
Ala Ala Phe Phe Ile Thr Tyr Glu Tyr Val Lys Trp Phe Leu His Ala
50 55 60
Asp Ser Ser Ser Tyr Leu Thr Pro Met Lys His Met Leu Ala Ala Ser
65 70 75
Ala Gly Glu Val Val Ala Cys Leu Ile Arg Val Pro Ser Glu Val Val
80 85 90 95
Lys Gln Arg Ala Gln Val Ser Ala Ser Thr Arg Thr Phe Gln Ile Phe
100 105 110
Ser Asn Ile Leu Tyr Glu Glu Gly Ile Gln Gly Leu Tyr Arg Gly Tyr
115 120 125
Lys Ser Thr Val Leu Arg Glu Ile Pro Phe Ser Leu Val Gln Phe Pro
130 135 140
Leu Trp Glu Ser Leu Lys Ala Leu Trp Ser Trp Arg Gln Asp His Val
145 150 155
Val Asp Ser Trp Gln Ser Ala Val Cys Gly Ala Phe Ala Gly Gly Phe
160 165 170 175
Ala Ala Ala Val Thr Thr Pro Leu Asp Val Ala Lys Thr Arg Ile Met
180 185 190
Leu Ala Lys Ala Gly Ser Ser Thr Ala Asp Gly Asn Val Leu Ser Val
195 200 205
Leu His Gly Val Trp Arg Ser Gln Gly Leu Ala Gly Leu Phe Ala Gly
210 215 220
Val Phe Pro Arg Met Ala Ala Ile Ser Leu Gly Gly Phe Ile Phe Leu
225 230 235
Gly Ala Tyr Asp Arg Thr His Ser Leu Leu Leu Glu Val Gly Arg Lys
240 245 250 255
Ser Pro

<210> 245
<211> 406
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35...-1

<400> 245
Met Arg Gly Ser Val Glu Cys Thr Trp Gly Trp Gly His Cys Ala Pro
-35 -30 -25 -20
Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly
-15 -10 -5

<400> 246
 Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Thr
 -15 -10 -5
 Pro Ser Ala Ser Val Ile Arg Thr
 1 5

<210> 247
 <211> 348
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 247
 Met Ala Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met
 -25 -20 -15
 Leu Leu Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His
 -10 -5 1
 Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr
 5 10 15
 Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Leu Asp Ala
 20 25 30 35
 Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
 40 45 50
 Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
 55 60 65
 Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
 70 75 80
 Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
 85 90 95
 Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
 100 105 110 115
 Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
 120 125 130
 Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
 135 140 145
 Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
 150 155 160
 Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
 165 170 175
 Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser
 180 185 190 195
 Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
 200 205 210
 Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser
 215 220 225
 Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys
 230 235 240
 Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys
 245 250 255
 Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln
 260 265 270 275
 Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val
 280 285 290
 Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu
 295 300 305

Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
 310 315

<210> 248
 <211> 397
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36..-1

<400> 248
 Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys Phe
 -35 -30 -25
 Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
 -20 -15 -10 -5
 Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135 140
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser Pro
 190 195 200
 Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp Glu
 205 210 215 220
 Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser Val
 225 230 235
 Gln Glu Asp Ser Glu Ser Pro Ser Pro Glu Asp Ile Pro Asp Tyr Leu
 240 245 250
 Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr Glu
 255 260 265
 Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala Arg
 270 275 280
 Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile Lys
 285 290 295 300
 Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys Ile
 305 310 315
 Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg Glu

320 325 330
 Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile Lys
 335 340 345
 Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
 350 355 360

<210> 249
 <211> 403
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 249
 Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
 -20 -15 -10
 Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly
 -5 1 5 10
 Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu
 15 20 25
 Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
 30 35 40
 Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
 45 50 55
 Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
 60 65 70 75
 Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
 80 85 90
 Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
 95 100 105
 Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
 110 115 120
 Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
 125 130 135
 Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
 140 145 150 155
 Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Val
 160 165 170
 Ser Glu Tyr Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys
 175 180 185
 Arg Ile Gln Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr
 190 195 200
 Gly Leu Arg Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile
 205 210 215
 Gly Val Ala Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser
 220 225 230 235
 Tyr Met Gln Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser
 240 245 250
 Leu Gln Val Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln
 255 260 265
 Arg Arg Ile Ser Ala His Gln Pro Gly Ala Gly Pro Glu Gly Gln Glu
 270 275 280
 Glu Ser Thr Pro Gln Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu
 285 290 295
 Asp Pro Ser Gly Thr Glu Gly Gln Leu Ser Glu Glu Glu Lys Pro Asp
 300 305 310 315

<211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 252
 Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu
 -15 -10 -5 1
 Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala
 5 10 15
 Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala
 20 25 30
 Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser
 35 40 45
 Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu
 50 55 60 65
 Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
 70 75 80
 Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
 85 90 95
 Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu
 100 105 110
 Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala
 115 120

<210> 253
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<220>
 <221> UNSURE
 <222> 45
 <223> Xaa = Glu,Gln

<220>
 <221> UNSURE
 <222> 44
 <223> Xaa = Lys,Asn

<400> 253
 Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe
 -30 -25 -20
 Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys
 -15 -10 -5 1
 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn
 35 40 45

Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser
 50 55 60 65
 Trp Thr Leu Ser Leu Leu Leu Thr Gly Phe Leu Ser
 70 75

<210> 254
 <211> 147
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<400> 254
 Met Val Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu
 -20 -15 -10
 Gly Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His
 -5 1 5
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 10 15 20
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 25 30 35 40
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile
 45 50 55
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
 60 65 70
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
 75 80 85
 Trp Pro Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val
 90 95 100
 Val Ala Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe
 105 110 115 120
 Arg Arg Pro

<210> 255
 <211> 381
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 255
 Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser
 -30 -25 -20
 Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln
 -15 -10 -5
 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met

65	70	75
Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys		
80	85	90
Ser Lys Asp Tyr Phe Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr		
	100	105
Ala Gly Ala Arg Gln Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln		
	115	120
Arg Asn Val Ala Ile Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr		
	130	135
Ser Pro His Cys Lys Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu		
	145	150
Thr Tyr Val Ala Trp Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile		
160	165	170
Gly Ser Gly Cys Asn Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly		
	180	185
Gln Lys Leu Gly Ile His Ser Glu Ser Cys His Gly Trp Ile Leu Gly		
	195	200
Glu His Gly Asp Ser Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala		
	210	215
Gly Val Pro Leu Lys Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp		
	225	230
Pro Glu Gln Trp Lys Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr		
240	245	250
Glu Ile Ile Lys Met Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser		
	260	265
Val Ala Asp Leu Thr Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His		
	275	280
Pro Val Ser Thr Ile Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val		
	290	295
Phe Leu Ser Ile Pro Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu		
	305	310
Ile Lys Ile Lys Leu Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser		
320	325	330
Ala Lys Thr Leu Trp Glu Ile Gln Asn Lys Leu Lys Leu		
	340	345

<210> 256

<211> 139

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -33...-1

<400> 256

Met Ser Trp Thr Val Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser		
	-30	-25
Val Gly Ala Asn Phe Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln		
	-15	-10
Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser		
1	5	10
Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu		
	20	25
Lys Pro Val His His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val		
	35	40
Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu		
	50	55
		60

Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
65 70 75
Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val
80 85 90 95
Ala Lys Ile Thr Leu Ser Gln Gln Thr Pro Thr
100 105

<210> 257
<211> 265
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14...-1

<400> 257
Met Asn Phe Ile Leu Phe Ile Phe Ile Pro Gly Val Phe Ser Leu Lys
-10 -5 1
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
5 10 15
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
20 25 30
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
35 40 45 50
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
55 60 65
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
70 75 80
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
85 90 95
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
100 105 110
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
115 120 125 130
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
135 140 145
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
150 155 160
Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser
165 170 175
Val Asn Pro Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly
180 185 190
Val Ser Asp Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu
195 200 205 210
Gly Thr Thr Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu
215 220 225
Ser Lys Ile Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met
230 235 240
His Glu Asn Asp Glu Ser Val Thr Arg
245 250

<210> 258
<211> 200
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -20...-1

<400> 258

Met	Asp	Ser	Ser	Thr	Ala	His	Ser	Pro	Val	Phe	Leu	Val	Phe	Pro	Pro
-20					-15					-10					-5
Glu	Ile	Thr	Ala	Ser	Glu	Tyr	Glu	Ser	Thr	Glu	Leu	Ser	Ala	Thr	Thr
			1				5						10		
Phe	Ser	Thr	Gln	Ser	Pro	Leu	Gln	Lys	Leu	Phe	Ala	Arg	Lys	Met	Lys
	15					20						25			
Ile	Leu	Gly	Thr	Ile	Gln	Ile	Leu	Phe	Gly	Ile	Met	Thr	Phe	Ser	Phe
	30				35					40					
Gly	Val	Ile	Phe	Leu	Phe	Thr	Leu	Leu	Lys	Pro	Tyr	Pro	Arg	Phe	Pro
45					50					55					60
Phe	Ile	Phe	Leu	Ser	Gly	Tyr	Pro	Phe	Trp	Gly	Ser	Val	Leu	Phe	Ile
			65					70						75	
Asn	Ser	Gly	Ala	Phe	Leu	Ile	Ala	Val	Lys	Arg	Lys	Thr	Thr	Glu	Thr
			80					85					90		
Leu	Ile	Ile	Leu	Ser	Arg	Ile	Met	Asn	Phe	Leu	Ser	Ala	Leu	Gly	Ala
		95					100					105			
Ile	Ala	Gly	Ile	Ile	Leu	Leu	Thr	Phe	Gly	Phe	Ile	Leu	Asp	Gln	Asn
	110					115					120				
Tyr	Ile	Cys	Gly	Tyr	Ser	His	Gln	Asn	Ser	Gln	Cys	Lys	Ala	Val	Thr
125					130					135					140
Val	Leu	Phe	Leu	Gly	Ile	Leu	Ile	Thr	Leu	Met	Thr	Phe	Ser	Ile	Ile
			145						150					155	
Glu	Leu	Phe	Ile	Ser	Leu	Pro	Phe	Ser	Ile	Leu	Gly	Cys	His	Ser	Glu
			160					165					170		
Asp	Cys	Asp	Cys	Glu	Gln	Cys	Cys								
		175					180								

<210> 259

<211> 394

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39...-1

<400> 259

Met	Ala	Thr	Ala	Gln	Leu	Gln	Arg	Thr	Pro	Met	Ser	Ala	Leu	Val	Phe
				-35					-30					-25	
Pro	Asn	Lys	Ile	Ser	Thr	Glu	His	Gln	Ser	Leu	Val	Leu	Val	Lys	Arg
		-20						-15					-10		
Leu	Leu	Ala	Val	Ser	Val	Ser	Cys	Ile	Thr	Tyr	Leu	Arg	Gly	Ile	Phe
		-5				1				5					
Pro	Glu	Cys	Ala	Tyr	Gly	Thr	Arg	Tyr	Leu	Asp	Asp	Leu	Cys	Val	Lys
10					15				20					25	
Ile	Leu	Arg	Glu	Asp	Lys	Asn	Cys	Pro	Gly	Ser	Thr	Gln	Leu	Val	Lys
			30						35					40	
Trp	Ile	Leu	Gly	Cys	Tyr	Asp	Ala	Leu	Gln	Lys	Lys	Tyr	Leu	Arg	Met
			45					50					55		
Val	Val	Leu	Ala	Val	Tyr	Thr	Asn	Pro	Glu	Asp	Pro	Gln	Thr	Ile	Ser
		60					65					70			
Glu	Cys	Tyr	Gln	Phe	Lys	Phe	Lys	Tyr	Thr	Asn	Asn	Gly	Pro	Leu	Met
	75					80				85					
Asp	Phe	Ile	Ser	Lys	Asn	Gln	Ser	Asn	Glu	Ser	Ser	Met	Leu	Ser	Thr

90					95					100				105
Asp	Thr	Lys	Lys	Ala	Ser	Ile	Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile
				110					115					120
Met	Gln	Asn	Leu	Gly	Pro	Leu	Pro	Asn	Asp	Val	Cys	Leu	Thr	Met
			125					130					135	
Leu	Phe	Tyr	Tyr	Asp	Glu	Val	Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro
		140					145					150		
Phe	Lys	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro
	155					160				165				Met
Tyr	Leu	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys
170					175					180				185
Lys	Val	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr
			190						195					200
Leu	Ser	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg
			205					210					215	
Lys	Asp	Val	Glu	Asp	Glu	Gln	Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu
	220						225					230		Asp
Ile	Glu	Thr	Lys	Met	Glu	Glu	Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser
	235					240					245			Glu
Leu	Glu	Glu	Pro	Ser	Leu	Val	Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg
250					255					260				265
Lys	Glu	Ser	Pro	Asp	Leu	Ser	Ile	Ser	His	Ser	Gln	Val	Glu	Gln
				270					275					280
Val	Asn	Lys	Thr	Ser	Glu	Leu	Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg
		285					290					295		Ser
Gly	Lys	Val	Phe	Gln	Asn	Lys	Met	Ala	Asn	Gly	Asn	Gln	Pro	Val
	300						305					310		Lys
Ser	Ser	Lys	Glu	Asn	Arg	Lys	Arg	Ser	Gln	His	Glu	Ser	Gly	Arg
	315					320				325				Ile
Val	Leu	His	His	Phe	Asp	Ser	Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys
330					335					340				345
Arg	Lys	Phe	Ser	Glu	Pro	Lys	Glu	His	Ile					
			350					355						

<210> 260
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400>	260														
Met	Ala	Leu	Glu	Val	Leu	Met	Leu	Leu	Ala	Val	Leu	Ile	Trp	Thr	Gly
	-15						-10					-5			
Ala	Glu	Asn	Leu	His	Val	Lys	Ile	Ser	Cys	Ser	Leu	Asp	Trp	Leu	Met
1				5					10					15	
Val	Ser	Val	Ile	Pro	Val	Ala	Glu	Ser	Arg	Asn	Leu	Tyr	Ile	Phe	Ala
				20				25						30	
Asp	Glu	Leu	His	Leu	Gly	Met	Gly	Cys	Pro	Ala	Asn	Arg	Ile	His	Thr
		35					40					45			
Tyr	Val	Tyr	Glu	Phe	Ile	Tyr	Leu	Val	Arg	Asp	Cys	Gly	Ile	Arg	Thr
	50					55						60			
Arg	Val	Val	Ser	Glu	Glu	Thr	Leu	Leu	Phe	Gln	Thr	Glu	Leu	Tyr	Phe
	65				70					75					
Thr	Pro	Arg	Asn	Ile	Asp	His	Asp	Pro	Gln	Glu	Ile	His	Leu	Glu	Cys
80					85				90					95	

Ser Thr Ser Arg Lys Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn
 100 105 110
 Glu Ile Lys Leu Asp Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr
 115 120 125
 Ala Glu Glu Leu Gly Leu Leu Ser Ser Ser Pro Asn Leu Leu
 130 135 140

<210> 261
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 261
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys
 -30 -25 -20
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser
 -15 -10 -5
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu
 1 5 10 15
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp
 20 25 30
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg
 35 40 45
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu
 50 55 60
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys
 65 70 75 80
 Ser Phe Arg Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe
 85 90 95
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu
 100 105 110
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu
 115 120 125
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala
 130 135 140
 Leu Trp Glu Asp Lys Thr Ser Leu Trp Glu Glu Asn Ala Leu Trp
 145 150 155 160
 Glu Glu Glu Arg Ala Phe Trp Met Glu Asn Asn Gly His Ile Ala Gly
 165 170 175
 Glu Gln Met Leu Glu Asp Gly Pro His Asn Ala Asn Arg Gly Gln Arg
 180 185 190
 Leu Leu Ala Phe Ser Arg Gly Arg Ala
 195 200

<210> 262
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 262

Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
 -20 -15 -10 -5
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
 1 5 10
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 15 20 25
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu
 30 35 40
 Glu Pro Ser
 45

<210> 263
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25..-1

<400> 263
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser
 -25 -20 -15 -10
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro
 -5 1 5
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg
 10 15 20
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser
 25 30 35
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro
 40 45 50 55
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
 60 65

<210> 264
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19..-1

<400> 264
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
 -15 -10 -5
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
 1 5 10
 Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln
 15 20 25
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
 30 35 40 45
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys
 50 55 60
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu
 65 70 75
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln
 80 85 90

Leu Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu
 95 100 105
 His Leu Glu Gln Leu Ala Glu Tyr Leu Leu Ala Glu Glu Pro His Val
 110 115 120 125
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser
 130 135 140
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155

<210> 265
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 265
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
 -15 -10 -5
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
 1 5 10 15
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
 20 25 30
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
 35 40 45
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
 50 55 60
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln
 65 70 75
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe
 80 85

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 266
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 -15 -10 -5
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 1 5 10
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 15 20 25 30
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 35 40 45
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 50 55 60
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 65 70 75
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 80 85 90

Leu Gly Leu Gly Met Leu Leu Pro Pro Arg Leu Leu
 95 100 105

<210> 267

<211> 261

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -16...-1

<400> 267

Met	Glu	Asn	Phe	Ser	Leu	Leu	Ser	Ile	Ser	Gly	Pro	Pro	Ile	Ser	Ser
-15						-10					-5				
Ser	Ala	Leu	Ser	Ala	Phe	Pro	Asp	Ile	Met	Phe	Ser	Arg	Ala	Thr	Ser
1			5						10					15	
Leu	Pro	Asp	Ile	Ala	Lys	Thr	Ala	Val	Pro	Thr	Glu	Ala	Ser	Ser	Pro
			20					25					30		
Ala	Gln	Ala	Leu	Pro	Pro	Gln	Tyr	Gln	Ser	Ile	Ile	Val	Arg	Gln	Gly
		35					40					45			
Ile	Gln	Asn	Thr	Val	Leu	Ser	Pro	Asp	Cys	Ser	Leu	Gly	Asp	Thr	Gln
		50				55					60				
His	Gly	Glu	Lys	Leu	Arg	Arg	Asn	Cys	Thr	Ile	Tyr	Arg	Pro	Trp	Phe
65					70					75					80
Ser	Pro	Tyr	Ser	Tyr	Phe	Val	Cys	Ala	Asp	Lys	Glu	Ser	Gln	Leu	Glu
				85					90					95	
Ala	Tyr	Asp	Phe	Pro	Glu	Val	Gln	Gln	Asp	Glu	Gly	Lys	Trp	Asp	Asn
			100					105					110		
Cys	Leu	Ser	Glu	Asp	Met	Ala	Glu	Asn	Ile	Cys	Ser	Ser	Ser	Ser	Ser
		115					120					125			
Pro	Glu	Asn	Thr	Cys	Pro	Arg	Glu	Ala	Thr	Lys	Lys	Ser	Arg	His	Gly
		130				135						140			
Leu	Asp	Ser	Ile	Thr	Ser	Gln	Asp	Ile	Leu	Met	Ala	Ser	Arg	Trp	His
145					150					155					160
Pro	Ala	Gln	Gln	Asn	Gly	Tyr	Lys	Cys	Val	Ala	Cys	Cys	Arg	Met	Tyr
				165					170					175	
Pro	Thr	Leu	Asp	Phe	Leu	Lys	Ser	His	Ile	Lys	Arg	Gly	Phe	Arg	Glu
			180					185					190		
Gly	Phe	Ser	Cys	Lys	Val	Tyr	Tyr	Arg	Lys	Leu	Lys	Ala	Leu	Trp	Ser
		195					200					205			
Lys	Glu	Gln	Lys	Ala	Arg	Leu	Gly	Asp	Arg	Leu	Ser	Ser	Gly	Ser	Cys
	210					215					220				
Gln	Ala	Phe	Asn	Ser	Pro	Ala	Glu	His	Leu	Arg	Gln	Ile	Gly	Gly	Glu
225					230					235					240
Ala	Tyr	Leu	Cys	Leu											
				245											

<210> 268

<211> 76

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 268

Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu
 -25 -20 -15 -10
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr
 -5 1 5
 Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala Ser Arg Ser Ala Asp Gln
 10 15 20
 Ser Ser Gln Lys Val Lys Leu Arg Met Phe Thr Gly Arg Leu Pro Ile
 25 30 35
 Gly Pro Phe Ala Ser Val Gly Asn Ala Ala Glu Leu
 40 45 50

<210> 269
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 269
 Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val Leu Ala
 -15 -10 -5
 Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp
 1 5 10 15
 Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr
 20 25 30
 Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu
 35 40 45
 Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser
 50 55 60
 Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu
 65 70 75 80
 Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly
 85 90 95
 Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met
 100 105 110
 Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn Pro Gly
 115 120 125
 Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys Gln Phe
 130 135 140
 Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val Thr Ser
 145 150 155 160
 Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met Ser Trp
 165 170 175
 Leu Val Cys Gly Ser Lys Leu
 180

<210> 270
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 270

Met Ala Ser Val Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys
 -35 -30 -25
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser
 -20 -15 -10 -5
 Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys
 1 5 10
 Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser Gly Ile Thr Met Val Leu
 15 20 25
 Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys
 30 35 40
 His Glu Arg Leu Arg Lys Tyr His
 45 50

<210> 271
 <211> 481
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 271
 Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu
 -25 -20 -15 -10
 Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala
 -5 1 5
 Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu
 10 15 20
 Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly
 25 30 35
 Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser
 40 45 50 55
 Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val
 60 65 70
 Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val
 75 80 85
 Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser
 90 95 100
 Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu
 105 110 115
 Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser
 120 125 130 135
 Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp
 140 145 150
 Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val
 155 160 165
 Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp
 170 175 180
 Leu Gln Pro Tyr Leu Gln Thr Leu Thr Val Thr Thr Glu Ile Asp Ser
 185 190 195
 Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala
 200 205 210 215
 Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His
 220 225 230
 Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu
 235 240 245
 His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr

<212> PRT
<213> Homo sapiens

<400> 273
Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
1 5 10 15
Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
20 25 30
Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
35 40 45
His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
50 55 60
Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
65 70 75 80
Leu His

<210> 274
<211> 373
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27...-1

<400> 274
Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
-25 -20 -15
Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile
-10 -5 1 5
Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu
10 15 20
Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile
25 30 35
Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu
40 45 50
Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly
55 60 65
Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro
70 75 80 85
Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser
90 95 100
Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly
105 110 115
Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro
120 125 130
Pro Gly Gly Gly Glu Val Phe Ser Cys Pro Val Arg Lys Val
135 140 145
Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg
150 155 160 165
Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile
170 175 180
Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr
185 190 195
Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly
200 205 210
Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser
215 220 225

Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro
 230 235 240 245
 Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Glu Glu Ile Tyr
 250 255 260
 Arg Gly Gly Cys Val Asp Ser Thr Asn Gln Ser Leu Ala Leu Leu Leu
 265 270 275
 Met Thr Leu Gly Gln Gln Asp Val Ser Lys Val Leu Leu Gly Pro Leu
 280 285 290
 Ser Pro Tyr Thr Ile Glu Phe Leu Arg His Leu Lys Ser Phe Phe Gln
 295 300 305
 Ile Met Phe Lys Ile Glu Thr Lys Pro Cys Gly Glu Glu Leu Lys Gly
 310 315 320 325
 Gly Asp Lys Val Leu Met Thr Cys Val Gly Ile Gly Phe Ser Asn Leu
 330 335 340
 Ser Arg Thr Leu Lys
 345

<210> 275
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 275
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
 60 65

<210> 276
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 276
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
 -20 -15 -10 -5
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40

Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55 60
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
 65 70 75
 Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
 80 85 90
 Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
 95 100 105
 Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
 110 115 120
 Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
 125 130 135 140
 Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
 145 150 155
 Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
 160 165 170
 Leu Phe Ser Pro Ala
 175

<210> 277
 <211> 344
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 277
 Met Asp Phe Leu Val Leu Phe Leu Phe Tyr Leu Ala Ser Val Leu Met
 -25 -20 -15
 Gly Leu Val Leu Ile Cys Val Cys Ser Lys Thr His Ser Leu Lys Gly
 -10 -5 1
 Leu Ala Arg Gly Gly Ala Gln Ile Phe Ser Cys Ile Ile Pro Glu Cys
 5 10 15
 Leu Gln Arg Ala Val His Gly Leu Leu His Tyr Leu Phe His Thr Arg
 20 25 30 35
 Asn His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr
 40 45 50
 Thr Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu
 55 60 65
 Ser Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu
 70 75 80
 Phe Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys
 85 90 95
 Ala Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Val Met
 100 105 110 115
 Phe Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala
 120 125 130
 Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe Asp
 135 140 145
 His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg
 150 155 160
 Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val
 165 170 175
 Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp
 180 185 190 195
 Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met

Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys
		75					80					85			
Lys	Met	Asp	Glu	Leu	Tyr	Pro	Met	Glu	Pro	Glu	Glu	Glu	Ala	Asn	Gly
	90					95					100				
Ser	Glu	Ile	Leu	Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Lys	Asp	Ala
105					110					115					120
Glu	Glu	Asp	Asp	Ser	Leu	Ala	Asn	Ser	Ser	Asp	Leu	Leu	Lys	Glu	Leu
				125					130					135	
Leu	Glu	Thr	Gly	Asp	Asn	Arg	Glu	Arg	Ser	His	His	Gln	Asp	Gly	Ser
			140					145					150		
Asp	Asn	Glu	Glu	Glu	Val	Ser	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Gly
		155					160					165			
Leu	Lys	Arg	Ser	Pro	Gln	Leu	Glu	Asp	Glu	Ala	Lys	Glu	Leu	Gln	Lys
	170					175					180				
Arg	Tyr	Gly	Gly	Phe	Met	Arg	Arg	Val	Gly	Arg	Pro	Glu	Trp	Trp	Met
185					190					195					200
Asp	Tyr	Gln	Lys	Arg	Tyr	Gly	Gly	Phe	Leu	Lys	Arg	Phe	Ala	Glu	Ala
				205				210						215	
Leu	Pro	Ser	Asp	Glu	Glu	Gly	Glu	Ser	Tyr	Ser	Lys	Glu	Val	Pro	Glu
			220				225						230		
Met	Glu	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Phe					
		235					240								

<210> 280

<211> 362

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -40...-1

<400> 280

Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	Glu	Ser	Glu	Gly	Phe	Ala	Gly	Ser
-40					-35					-30					-25
Arg	Lys	Gly	Val	Leu	Gly	Arg	Val	Tyr	Glu	Thr	Val	Val	Met	Leu	Met
			-20						-15						-10
Leu	Leu	Thr	Leu	Leu	Val	Leu	Gly	Met	Val	Trp	Val	Ala	Ser	Ala	Ile
			-5					1				5			
Val	Asp	Lys	Asn	Lys	Ala	Asn	Arg	Glu	Ser	Leu	Tyr	Asp	Phe	Trp	Glu
	10				15						20				
Tyr	Tyr	Leu	Pro	Tyr	Leu	Tyr	Ser	Cys	Ile	Ser	Phe	Leu	Gly	Val	Leu
25					30					35					40
Leu	Leu	Leu	Val	Cys	Thr	Pro	Leu	Gly	Leu	Ala	Arg	Met	Phe	Ser	Val
			45					50						55	
Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	Leu	Leu	Glu	Asp	Leu	Glu	Glu
			60					65					70		
Gln	Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	Ala	Ala	Leu	Thr	Arg	Arg	Ile
		75					80					85			
Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	Leu	Asp	Met	Glu	Leu	Leu	His
	90					95					100				
Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	Arg	Val	Leu	Leu	Glu	Lys	Arg
105					110					115					120
Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	Leu	Gly	Tyr	Pro	Leu	Ala	Met
			125						130					135	
Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	Ser	Val	Leu	Ile	Val	Ala	Ile
			140					145						150	

His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met
 155 160 165
 Gln Gly Thr Ser Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe
 170 175 180
 Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser
 185 190 195 200
 Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg
 205 210 215
 Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu
 220 225 230
 Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu
 235 240 245
 Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly
 250 255 260
 Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr
 265 270 275 280
 Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Val Arg Ala Glu Leu
 285 290 295
 Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe
 300 305 310
 Pro Gln Ala Ser Arg Lys Thr Gln His Gln
 315 320

<210> 281
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 281
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
 -20 -15 -10
 Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln
 -5 1 5 10
 Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys
 15 20 25
 Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln
 30 35 40
 Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys
 45 50 55
 Ser
 60

<210> 282
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 282
 Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
 -25 -20 -15

09876997-060801

Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
	-10						-5					1			
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5					10					15					20
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
				25					30					35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45					50		
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
	55						60					65			
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70					75					80				
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90				95						100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105					110						115
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
	135						140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
				185					190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
			200					205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
	215						220						225		
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250				255						260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
				265					270					275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
			280					285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
	295						300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330				335						340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
			360					365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
	375						380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
				425					430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
			440					445					450		

Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
 455 460 465
 Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
 470 475 480
 Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
 485 490 495 500
 Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
 505 510

<210> 283
 <211> 468
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 283
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170
 Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala
 175 180 185
 Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser
 190 195 200
 Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser
 205 210 215
 Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu
 220 225 230 235
 Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly
 240 245 250
 Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser
 255 260 265
 Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro
 270 275 280
 Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile

285 290 295
 Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr
 300 305 310 315
 Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe
 320 325 330
 Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser
 335 340 345
 Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val
 350 355 360
 Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val
 365 370 375
 Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu
 380 385 390 395
 Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro
 400 405 410
 Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys
 415 420 425
 Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val
 430 435 440
 Ser Gln Pro Ser
 445

<210> 284
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 284
 Met Val Arg Ile Gln Arg Arg Lys Leu Leu Ala Ser Cys Leu Cys Val
 -30 -25 -20
 Thr Ala Thr Val Phe Leu Leu Val Thr Leu Gln Ala Leu Asp Thr Val
 -15 -10 -5 1
 Glu Asn Leu Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser
 5 10 15
 Met Gln Cys Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser
 20 25 30
 Glu His Ile Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys
 35 40 45
 Glu Phe Lys Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu
 50 55 60 65
 Ala Pro Thr His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe
 70 75 80
 Asn Arg Lys Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp
 85 90 95
 Trp Ser Pro Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala
 100 105 110
 Asp Ala Cys Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met
 115 120 125
 Thr Lys Ala Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu
 130 135 140 145
 Pro Leu Pro Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu
 150 155 160
 Ser Pro Lys Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu
 165 170 175

Phe Asn Tyr Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr
 180 185 190
 Thr Gln Tyr Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu
 195 200 205
 Val Pro Leu Gln Ser Lys Asn Lys Leu Arg Lys Arg Leu Ala Pro Leu
 210 215 220 225
 Val Tyr Val Gln Ser Tyr Cys Asp Pro Pro Ser Asp Arg Asp Ser Tyr
 230 235 240
 Val Arg Glu Leu Met Thr Tyr Ile Glu Val Asp Ser Tyr Gly Glu Cys
 245 250 255
 Leu Arg Asn Lys Asp Leu Pro Gln Gln Leu Lys Asn Pro Ala Ser Met
 260 265 270
 Asp Ala Asp Gly Phe Tyr Arg Ile Ile Ala Gln Tyr Lys Phe Ile Leu
 275 280 285
 Ala Phe Glu Asn Ala Val Cys Asp Asp Tyr Ile Thr Glu Lys Phe Trp
 290 295 300 305
 Arg Pro Leu Lys Leu Gly Val Val Pro Val Tyr Tyr Gly Ser Pro Ser
 310 315 320
 Ile Thr Asp Trp Leu Pro Ser Asn Lys Ser Ala Ile Leu Val Ser Glu
 325 330 335
 Phe Ser His Pro Arg Glu Leu Ala Ser Tyr Ile Arg Arg Leu Asp Ser
 340 345 350
 Asp Asp Arg Leu Tyr Glu Ala Tyr Val Glu Trp Lys Leu Lys Gly Arg
 355 360 365
 Ser Leu Thr Ser Asp Phe
 370 375

<210> 285

<211> 305

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 285

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25 -20 -15
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
 -10 -5 1 5
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
 10 15 20
 Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
 25 30 35
 Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
 40 45 50
 Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
 55 60 65 70
 Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
 75 80 85
 Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
 90 95 100
 Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
 105 110 115
 Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
 120 125 130
 Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala

135 140 145 150
 Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
 155 160 165
 Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
 170 175 180
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
 185 190 195
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
 200 205 210
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
 215 220 225 230
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
 235 240 245
 Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
 250 255 260
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
 265 270 275

Tyr

<210> 286
 <211> 442
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<220>
 <221> UNSURE
 <222> 132
 <223> Xaa = Pro,Arg

<400> 286
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170

Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala	
			175					180					185			
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser	
		190					195					200				
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser	
	205					210					215					
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu	
220					225					230					235	
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly	
				240					245					250		
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser	
			255					260					265			
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro	
		270					275					280				
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile	
	285					290					295					
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr	
300						305				310					315	
Arg	Glu	Glu	Leu	Gly	Gly	Ser	Pro	Ala	Gln	Val	Ser	Gly	Ala	Ser	Phe	
				320					325					330		
Ser	Ser	Leu	Arg	Gln	Ser	Val	Ala	Gly	Thr	Tyr	Ser	Ile	Ser	Ser	Ser	
			335					340					345			
Leu	Thr	Ala	Glu	Pro	Gly	Ser	Ala	Gly	Ala	Thr	Tyr	Thr	Cys	Gln	Val	
		350					355					360				
Thr	His	Ile	Ser	Leu	Glu	Glu	Pro	Leu	Gly	Ala	Ser	Thr	Gln	Val	Val	
	365					370					375					
Pro	Pro	Glu	Arg	Arg	Thr	Ala	Leu	Gly	Val	Ile	Phe	Ala	Ser	Ser	Leu	
380					385					390					395	
Phe	Leu	Leu	Ala	Leu	Met	Phe	Leu	Gly	Leu	Gln	Arg	Arg	Gln	Ala	Pro	
				400					405					410		
Thr	Gly	Leu	Gly	Leu	Leu	Gln	Ala	Glu	Arg							
			415					420								

<210> 287

<211> 286

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 287

Met	Asn	Pro	Ala	Ser	Asp	Gly	Gly	Thr	Ser	Glu	Ser	Ile	Phe	Asp	Leu	
			-45					-40					-35			
Asp	Tyr	Ala	Ser	Trp	Gly	Ile	Arg	Ser	Thr	Leu	Met	Val	Ala	Gly	Phe	
		-30					-25					-20				
Val	Phe	Tyr	Leu	Gly	Val	Phe	Val	Val	Cys	His	Gln	Leu	Ser	Ser	Ser	
	-15				-10						-5					
Leu	Asn	Ala	Thr	Tyr	Arg	Ser	Leu	Val	Ala	Arg	Glu	Lys	Val	Phe	Trp	
1			5					10					15			
Asp	Leu	Ala	Ala	Thr	Arg	Ala	Val	Phe	Gly	Val	Gln	Ser	Thr	Ala	Ala	
		20						25					30			
Gly	Leu	Trp	Ala	Leu	Leu	Gly	Asp	Pro	Val	Leu	His	Ala	Asp	Lys	Ala	
		35				40					45					
Arg	Gly	Gln	Gln	Asn	Trp	Cys	Trp	Phe	His	Ile	Thr	Thr	Ala	Thr	Gly	
	50					55				60						
Phe	Phe	Cys	Phe	Glu	Asn	Val	Ala	Val	His	Leu	Ser	Asn	Leu	Ile	Phe	

65					70					75					80
Arg	Thr	Phe	Asp	Leu	Phe	Leu	Val	Ile	His	His	Leu	Phe	Ala	Phe	Leu
				85					90					95	
Gly	Phe	Leu	Gly	Cys	Leu	Val	Asn	Leu	Gln	Ala	Gly	His	Tyr	Leu	Ala
			100					105					110		
Met	Thr	Thr	Leu	Leu	Leu	Glu	Met	Ser	Thr	Pro	Phe	Thr	Cys	Val	Ser
		115					120					125			
Trp	Met	Leu	Leu	Lys	Ala	Gly	Trp	Ser	Glu	Ser	Leu	Phe	Trp	Lys	Leu
	130					135					140				
Asn	Gln	Trp	Leu	Met	Ile	His	Met	Phe	His	Cys	Arg	Met	Val	Leu	Thr
145					150					155				160	
Tyr	His	Met	Trp	Trp	Val	Cys	Phe	Trp	His	Trp	Asp	Gly	Leu	Val	Ser
			165					170					175		
Ser	Leu	Tyr	Leu	Pro	His	Leu	Thr	Leu	Phe	Leu	Val	Gly	Leu	Ala	Leu
			180					185					190		
Leu	Thr	Leu	Ile	Ile	Asn	Pro	Tyr	Trp	Thr	His	Lys	Lys	Thr	Gln	Gln
		195					200					205			
Leu	Leu	Asn	Pro	Val	Asp	Trp	Asn	Phe	Ala	Gln	Pro	Glu	Ala	Lys	Ser
	210					215					220				
Arg	Pro	Glu	Gly	Asn	Gly	Gln	Leu	Leu	Arg	Lys	Lys	Arg	Pro		
225					230					235					

<210> 288
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 288															
Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
	-20					-15					-10				
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1				5				10		
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu	
			15					20				25			
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
		30					35					40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
	45					50				55					
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65				70					75	
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
				80					85				90		
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
			95				100					105			
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
	110					115						120			
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
	125					130				135					
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140					145				150					155	
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr
			160					165					170		
Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln
			175					180					185		

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 290

Met	Ala	Val	Gly	Gly	Gly	Leu	Ala	Val	Ala	Gly	Leu	Pro	Ala	Leu	Gly
-20					-15					-10					-5
Phe	Thr	Gly	Ala	Gly	Ile	Ala	Ala	Asn	Ser	Val	Ala	Ala	Ser	Leu	Met
				1				5					10		
Ser	Trp	Ser	Ala	Ile	Leu	Asn	Gly	Gly	Gly	Val	Pro	Ala	Gly	Gly	Leu
		15					20					25			
Val	Ala	Thr	Leu	Gln	Ser	Leu	Gly	Ala	Gly	Gly	Ser	Ser	Val	Val	Ile
	30					35					40				
Gly	Asn	Ile	Gly	Ala	Leu	Met	Gly	Tyr	Ala	Thr	His	Lys	Tyr	Leu	Asp
45					50					55					60
Ser	Glu	Glu	Asp	Glu	Glu										
					65										

<210> 291
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 291

Met	Ala	Pro	Phe	Glu	Pro	Leu	Ala	Ser	Gly	Ile	Leu	Leu	Leu	Leu	Trp
		-20						-15					-10		
Leu	Ile	Ala	Pro	Ser	Arg	Ala	Cys	Thr	Cys	Val	Pro	Pro	His	Pro	Gln
		-5					1				5				
Thr	Ala	Phe	Cys	Asn	Ser	Asp	Leu	Val	Ile	Arg	Ala	Lys	Phe	Val	Gly
10					15					20				25	
Thr	Pro	Glu	Val	Asn	Gln	Thr	Thr	Leu	Tyr	Gln	Arg	Tyr	Glu	Ile	Lys
				30				35						40	
Met	Thr	Lys	Met	Tyr	Lys	Gly	Phe	Gln	Ala	Leu	Gly	Asp	Ala	Ala	Asp
			45					50					55		
Ile	Arg	Phe	Val	Tyr	Thr	Pro	Ala	Met	Glu	Ser	Val	Cys	Gly	Tyr	Phe
		60					65					70			
His	Arg	Ser	His	Asn	Arg	Ser	Glu	Glu	Phe	Leu	Ile	Ala	Gly	Lys	Leu
		75				80					85				
Gln	Asp	Gly	Leu	Leu	His	Ile	Thr	Thr	Cys	Ser	Phe	Val	Ala	Pro	Trp
90					95					100					105
Asn	Ser	Leu	Ser	Leu	Ala	Gln	Arg	Arg	Gly	Phe	Thr	Lys	Thr	Tyr	Thr
				110					115					120	
Val	Gly	Cys	Glu	Glu	Cys	Thr	Val	Phe	Pro	Cys	Leu	Ser	Phe	Pro	Cys
			125					130					135		
Lys	Leu	Gln	Ser	Gly	Thr	His	Cys	Leu	Trp	Thr	Asp	Gln	Leu	Leu	Gln
		140					145					150			
Gly	Ser	Glu	Lys	Gly	Phe	Gln	Ser	Arg	His	Leu	Ala	Cys	Leu	Pro	Arg
	155					160					165				
Glu	Pro	Gly	Leu	Cys	Thr	Trp	Gln	Ser	Leu	Arg	Ser	Gln	Ile	Ala	
170						175					180				

<210> 292
 <211> 111

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 292
Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser
-20 -15 -10
Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile
-5 1 5
Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg
10 15 20
Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys
25 30 35 40
Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys
45 50 55
Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr
60 65 70
Leu Met Val Ile Gln Asp Ile Thr Ala Met Val Arg Phe Asn Ile
75 80 85

<210> 293
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 293
Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu
-15 -10 -5 1
Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys
5 10 15
Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val
20 25 30
Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met
35 40 45
Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp
50 55 60 65
Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe
70 75 80
Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys
85 90 95
Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr
100 105 110
Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
115 120

<210> 294
<211> 160
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -27...-1

<400> 294

Met	Gln	Arg	Val	Ser	Gly	Leu	Leu	Ser	Trp	Thr	Leu	Ser	Arg	Val	Leu
	-25						-20					-15			
Trp	Leu	Ser	Gly	Leu	Ser	Glu	Pro	Gly	Ala	Ala	Arg	Gln	Pro	Arg	Ile
	-10					-5					1			5	
Met	Glu	Glu	Lys	Ala	Leu	Glu	Val	Tyr	Asp	Leu	Ile	Arg	Thr	Ile	Arg
			10						15					20	
Asp	Pro	Glu	Lys	Pro	Asn	Thr	Leu	Glu	Glu	Leu	Glu	Val	Val	Ser	Glu
			25					30					35		
Ser	Cys	Val	Glu	Val	Gln	Glu	Ile	Asn	Glu	Glu	Glu	Tyr	Leu	Val	Ile
		40					45					50			
Ile	Arg	Phe	Thr	Pro	Thr	Val	Pro	His	Cys	Ser	Leu	Ala	Thr	Leu	Ile
	55					60					65				
Gly	Leu	Cys	Leu	Arg	Val	Lys	Leu	Gln	Arg	Cys	Leu	Pro	Phe	Lys	His
70					75					80					85
Lys	Leu	Glu	Ile	Tyr	Ile	Ser	Glu	Gly	Thr	His	Ser	Thr	Glu	Glu	Asp
				90					95					100	
Ile	Asn	Lys	Gln	Ile	Asn	Asp	Lys	Glu	Arg	Val	Ala	Ala	Ala	Met	Glu
			105					110					115		
Asn	Pro	Asn	Leu	Arg	Glu	Ile	Val	Glu	Gln	Cys	Val	Leu	Glu	Pro	Asp
		120					125						130		

<210> 295
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 295

Met	Pro	Pro	Phe	Leu	Leu	Leu	Thr	Cys	Leu	Phe	Ile	Thr	Gly	Thr	Ser
	-15					-10					-5				
Val	Ser	Pro	Val	Ala	Leu	Asp	Pro	Cys	Ser	Ala	Tyr	Ile	Ser	Leu	Asn
1			5					10						15	
Glu	Pro	Trp	Arg	Asn	Thr	Asp	His	Gln	Leu	Asp	Glu	Ser	Gln	Gly	Pro
			20					25					30		
Pro	Leu	Cys	Asp	Asn	His	Val	Asn	Gly	Glu	Trp	Tyr	His	Phe	Thr	Gly
		35					40					45			
Met	Ala	Gly	Asp	Ala	Met	Pro	Thr	Phe	Cys	Ile	Pro	Glu	Asn	His	Cys
	50					55					60				
Gly	Thr	His	Ala	Pro	Val	Trp	Leu	Asn	Gly	Ser	His	Pro	Leu	Glu	Gly
65					70					75					80
Asp	Gly	Ile	Val	Gln	Arg	Gln	Ala	Cys	Ala	Ser	Phe	Asn	Gly	Asn	Cys
				85					90					95	
Cys	Leu	Trp	Asn	Thr	Thr	Val	Glu	Val	Lys	Ala	Cys	Pro	Gly	Gly	Tyr
			100					105					110		
Tyr	Val	Tyr	Arg	Leu	Thr	Lys	Pro	Ser	Val	Cys	Phe	His	Val	Tyr	Cys
		115					120					125			
Gly	Arg	Glu	Tyr	Leu	Pro	Cys	Ala	Leu	Phe	Leu	His	Gln	Gln	Gly	His
	130					135					140				
Arg	Trp	Ser	Pro	Lys	Val	Pro	Asn	Tyr	Arg	Ile	Cys	Ser	Tyr	Ser	Gly
145					150					155					160
Asn	Tyr	Ile	Ser	Ile											

165

<210> 296
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<400> 296

Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser
-15 -10 -5
Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser Ile Ala
1 5 10
Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr
15 20 25 30
Cys Cys Ala Pro Gln Pro Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly
35 40 45
Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro
50 55 60
Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu
65 70 75
Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser
80 85 90
Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu
95 100 105 110
Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val
115 120 125
Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser
130 135 140
Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His
145 150 155
Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp
160 165 170
Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu
175 180 185 190
Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu
195 200 205
Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly
210 215 220
Trp Thr Thr Trp Ala Arg Trp
225

<210> 297
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41...-1

<400> 297

Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
-40 -35 -30
Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser

[illegible][illegible][illegible][illegible][illegible][illegible]

Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
			185						190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200						205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
		215					220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235						240			
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250					255					260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
				265					270					275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
		280						285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
		295					300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Leu	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
		360						365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
		375					380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
				425					430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
			440					445					450		
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro
	455						460					465			
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr
	470					475					480				
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg
485					490					495					500
Thr	Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr			
				505					510						

<210> 301

<211> 287

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -17...-1

<400> 301

Met	Glu	Leu	Glu	Arg	Ile	Val	Ser	Ala	Ala	Leu	Leu	Ala	Phe	Val	Gln
	-15						-10					-5			
Thr	His	Leu	Pro	Glu	Ala	Asp	Leu	Ser	Gly	Leu	Asp	Glu	Val	Ile	Phe
1				5					10					15	
Ser	Tyr	Val	Leu	Gly	Val	Leu	Glu	Asp	Leu	Gly	Pro	Ser	Gly	Pro	Ser
			20						25					30	
Glu	Glu	Asn	Phe	Asp	Met	Glu	Ala	Phe	Thr	Glu	Met	Met	Glu	Ala	Tyr
			35					40					45		
Val	Pro	Gly	Phe	Ala	His	Ile	Pro	Arg	Gly	Thr	Ile	Gly	Asp	Met	Met
	50						55					60			
Gln	Lys	Leu	Ser	Gly	Gln	Leu	Ser	Asp	Ala	Arg	Asn	Lys	Glu	Asn	Leu
65						70					75				
Gln	Pro	Gln	Ser	Ser	Gly	Val	Gln	Gly	Gln	Val	Pro	Ile	Ser	Pro	Glu
80					85					90					95
Pro	Leu	Gln	Arg	Pro	Glu	Met	Leu	Lys	Glu	Glu	Thr	Arg	Ser	Ser	Ala
				100					105					110	
Ala	Ala	Ala	Ala	Asp	Thr	Gln	Asp	Glu	Ala	Thr	Gly	Ala	Glu	Glu	Glu
			115					120					125		
Leu	Leu	Pro	Gly	Val	Asp	Val	Leu	Leu	Glu	Val	Phe	Pro	Thr	Cys	Ser
		130					135					140			
Val	Glu	Gln	Ala	Gln	Trp	Val	Leu	Ala	Lys	Ala	Arg	Gly	Asp	Leu	Glu
	145					150					155				
Glu	Ala	Val	Gln	Met	Leu	Val	Glu	Gly	Lys	Glu	Glu	Gly	Pro	Ala	Ala
160					165					170					175
Trp	Glu	Gly	Pro	Asn	Gln	Asp	Leu	Pro	Arg	Arg	Leu	Arg	Gly	Pro	Gln
				180					185					190	
Lys	Asp	Glu	Leu	Lys	Ser	Phe	Ile	Leu	Gln	Lys	Tyr	Met	Met	Val	Asp
		195						200					205		
Ser	Ala	Glu	Asp	Gln	Lys	Ile	His	Arg	Pro	Met	Ala	Pro	Lys	Glu	Ala
	210						215					220			
Pro	Lys	Lys	Leu	Ile	Arg	Tyr	Ile	Asp	Asn	Gln	Val	Val	Ser	Thr	Lys
	225					230					235				
Gly	Glu	Arg	Phe	Lys	Asp	Val	Arg	Asn	Pro	Glu	Ala	Glu	Glu	Met	Lys
240					245					250					255
Ala	Thr	Tyr	Ile	Asn	Leu	Lys	Pro	Ala	Arg	Lys	Tyr	Arg	Phe	His	
				260					265					270	

<210> 302

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 302

Met	Met	Arg	Cys	Cys	Arg	Arg	Arg	Cys	Cys	Cys	Arg	Gln	Pro	Pro	His
-35					-30					-25					-20
Ala	Leu	Arg	Pro	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	Pro	Pro	Leu	
				-15				-10					-5		
Ala	Ala	Ala	Ala	Ala	Gly	Pro	Asn	Arg	Cys	Asp	Thr	Ile	Tyr	Gln	Gly
			1			5					10				
Phe	Ala	Glu	Cys	Leu	Ile	Arg	Leu	Gly	Asp	Ser	Met	Gly	Arg	Gly	Gly
15						20					25				

Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala Cys Ala
 30 35 40 45
 Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val Trp Glu
 50 55 60
 Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn Leu His
 65 70 75
 Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr Gly Ser
 80 85 90
 Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu Pro Met
 95 100 105
 Ala Pro Ala Pro Pro Leu Leu Ala Ala Ala Leu Ala Leu Ala Tyr Leu
 110 115 120 125
 Leu Arg Pro Leu Ala
 130

<210> 303
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 303
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
 60 65 70
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
 75 80 85
 Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys
 90 95 100
 Thr Phe Val His Val Val Pro Ala Lys Pro Glu Gly Thr Phe Lys Leu
 105 110 115
 Val Ala Met Leu
 120

<210> 304
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 304
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20

Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr
-15 -10 -5
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
1 5 10
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
15 20 25 30
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr
35 40 45
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
50 55 60
Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
65 70 75
Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
80 85 90
Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
95 100 105 110
Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
115 120 125
Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
130 135 140
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
145 150 155
Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
160 165 170
Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
175 180 185 190
Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
195 200 205
Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
210 215 220
Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
225 230 235
Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
240 245 250
Asn Met Ser
255

<210> 305

<211> 81

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -49..-1

<400> 305

Met Glu Gly Ala Gly Ala Gly Ser Gly Phe Arg Lys Glu Leu Val Ser
-45 -40 -35
Arg Leu Leu His Leu His Phe Lys Asp Asp Lys Thr Lys Val Ser Gly
-30 -25 -20
Asp Ala Leu Gln Leu Met Val Glu Leu Leu Lys Val Phe Val Val Glu
-15 -10 -5
Ala Ala Val Arg Gly Val Arg Gln Ala Gln Ala Glu Asp Ala Leu Arg
1 5 10 15
Val Asp Val Asp Gln Leu Glu Lys Val Leu Pro Gln Leu Leu Leu Asp
20 25 30
Phe

<210> 306
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 306
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp
 -10 -5 1
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val
 70 75 80
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly
 85 90 95
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala
 100 105 110
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile
 115 120 125 130
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu
 135 140 145
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu
 150 155 160
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu
 165 170 175
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu
 180 185 190
 Ile Asn Lys Ser Gly Glu Lys Ala Met
 195 200

<210> 307
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 307
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25

Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 45 50 55 60
 Ile Leu Asn Gly Gly
 65

<210> 308
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 308
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys
 -40 -35 -30
 Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly
 -25 -20 -15
 Ser Leu Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr
 -10 -5 1 5
 Ser Ser Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys
 10 15 20
 Leu Gly Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys
 25 30 35
 Glu Asp Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro
 40 45 50
 Pro Leu Lys Ser Glu Lys His Glu Glu
 55 60

<210> 309
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 309
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20
 Lys Arg Ile Ala Tyr Phe Leu Cys Leu Ser Ala Leu Leu Leu Thr
 -15 -10 -5
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
 1 5 10
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
 15 20 25 30
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Val Phe Thr
 35 40 45
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
 50 55 60
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
 65 70 75
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
 80 85 90

09876997 050804

Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
 95 100 105 110
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
 115 120 125
 Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
 130 135 140
 Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
 145 150 155
 Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
 160 165 170
 Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
 175 180 185 190
 Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
 195 200 205
 Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
 210 215 220
 Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
 225 230 235
 Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
 240 245 250
 Asn Met Ser
 255

<210> 310

<211> 426

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -28...-1

<400> 310

Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
 -25 -20 -15
 Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
 -10 -5 1
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
 5 10 15 20
 His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro
 25 30 35
 Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
 40 45 50
 Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
 55 60 65
 Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
 70 75 80
 Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
 85 90 95 100
 Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
 105 110 115
 Lys Leu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
 120 125 130
 Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
 135 140 145
 Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
 150 155 160
 Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn

Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly
 145 150 155 160
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
 290 295 300
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Gly
 305 310 315 320
 Phe Gln Gln Arg Ala Leu Cys His Ala Leu Thr Phe Pro Ser Leu Gln
 325 330 335
 Arg Leu Val Tyr Ser Thr Cys Ser Leu Cys Gln Glu Glu Asn Glu Asp
 340 345 350
 Val Val Arg Asp Ala Leu Gln Gln Asn Pro Gly Ala Phe Arg Leu Ala
 355 360 365
 Pro Ala Leu Pro Ala Trp Pro His Arg Gly Leu Ser Thr Phe Pro Gly
 370 375 380
 Ala Glu His Cys Leu Arg Ala Ser Pro Glu Thr Thr Leu Ser Ser Gly
 385 390 395 400
 Phe Phe Val Ala Val Ile Glu Arg Val Glu Val Pro Ser Ser Ala Ser
 405 410 415
 Gln Ala Lys Ala Ser Ala Pro Glu Arg Thr Pro Ser Pro Ala Pro Lys
 420 425 430
 Arg Lys Lys Arg Gln Gln Arg Ala Ala Ala Gly Ala Cys Thr Pro Pro
 435 440 445
 Cys Thr
 450

<210> 312
 <211> 382
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 312
 Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
 -15 -10 -5
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
 1 5 10 15
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala

Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys
	35						40					45			
Lys	Leu	Arg	Pro	His	Leu	Ala	Lys	Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu
	50					55					60				
Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly
65					70					75					80
Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	Glu	Leu	Ala	Arg	Leu	Lys	Val	His
				85					90					95	
Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp	Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro
			100					105					110		
Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	Phe	Val	Arg	Val	Asn	Thr	Leu	Lys
		115					120					125			
Thr	Cys	Ser	Asp	Asp	Val	Val	Asp	Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser
	130					135					140				
Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu	Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly
145					150					155					160
Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	Met	Pro	Glu	Leu	Leu	Val	Phe	Pro
				165					170					175	
Ala	Gln	Thr	Asp	Leu	His	Glu	His	Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu
			180					185					190		
Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro
		195					200					205			
Pro	Pro	Gly	Ser	His	Val	Ile	Asp	Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys
	210					215					220				
Thr	Ser	His	Leu	Ala	Ala	Leu	Leu	Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala
225					230					235					240
Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala
				245					250					255	
Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala
			260					265					270		
Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	His	Glu	Val	His	Tyr	Ile	Leu	Leu
		275					280					285			
Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly	Met	Pro	Ser	Arg	Gln	Leu	Glu	Glu
	290					295					300				
Pro	Gly	Ala	Gly	Thr	Pro	Ser	Pro	Val	Arg	Leu	His	Ala	Leu	Ala	Ala
305					310					315					320
Ser	Ser	Ser	Glu	Pro	Cys	Ala	Thr	Arg	Ser	Leu	Ser	Leu	Pro	Cys	Ser
				325					330					335	
Gly	Ser	Ser	Thr	Pro	Arg	Ala	Pro	Ser	Ala	Arg	Arg	Arg	Met	Lys	Thr
			340					345					350		
Trp	Cys	Glu	Met	Arg	Cys	Ser	Arg	Thr	Arg	Ala	Pro	Ser	Gly		
		355					360					365			

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<210> 313
<211> 258
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -36..-1
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<400> 313
Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Glu Leu Arg Leu Cys Phe
   -35               -30             -25
Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp Ala
-20              -15                -10                 -5
```


Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135 140
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro Pro
 190 195 200
 Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly Ala
 205 210 215 220
 Arg Arg

<210> 314
 <211> 280
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 314
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu Pro
 -30 -25 -20
 Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
 -15 -10 -5
 Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val Val
 1 5 10 15
 His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu Tyr
 20 25 30
 Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu Phe
 35 40 45
 Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly Phe
 50 55 60
 Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val His
 65 70 75
 Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu Ser
 80 85 90 95
 Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser Pro
 100 105 110

Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro
 115 120 125
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu Ile
 130 135 140
 Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn Phe
 145 150 155
 Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly Val
 160 165 170 175
 Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn Glu
 180 185 190
 Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser Phe
 195 200 205
 Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro Met
 210 215 220
 Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr Glu
 225 230 235
 Thr Cys Ile Glu Pro Trp Leu Ser
 240 245

<210> 315
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 315
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu Pro
 -30 -25 -20
 Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu Leu
 -15 -10 -5
 Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val Val
 1 5 10 15
 His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu Tyr
 20 25 30
 Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu Phe
 35 40 45
 Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly Phe
 50 55 60
 Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val His
 65 70 75
 Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu Ser
 80 85 90 95
 Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser Pro
 100 105 110
 Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro
 115 120 125
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro
 130 135 140

<210> 316
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>

150		155		160
Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn				
165		170		175
Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly				180
	185		190	195
Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln				
	200		205	210
Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val				
	215		220	225
Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met				
	230		235	240
Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala				
245		250		255
Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu				260
	265		270	275
Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg				
	280		285	290
Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp				
	295		300	305
Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu				
	310		315	320
Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala				
325		330		335
Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe				
	345		350	355
Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu				
	360		365	370
Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile				
	375		380	385
Val Thr Glu Ile Ser Glu Glu Ser Gly Glu				
390		395		

<210> 318
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 318

Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val				
-20		-15		-10
Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln				-5
	1		5	10
Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg				
	15		20	25
Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile				
30		35		40
Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu				
45		50		55
Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe				
	65		70	75
Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met				
	80		85	90
Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln				
95		100		105

Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val
 110 115 120
 Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly
 125 130 135 140
 Lys Arg Leu Pro Thr Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly
 145 150 155
 Leu Lys Gly Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg
 160 165 170
 Thr Asn Leu Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp
 175 180 185
 Gly Phe His Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn
 190 195 200
 Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
 205 210 215 220
 Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser
 225 230 235
 Trp Ile Asp Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr
 240 245 250
 Thr Arg Met Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe
 255 260 265
 Arg Cys Ala Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu
 270 275 280

<210> 319
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 319
 Met Gly Ser Gly Trp Leu Thr Ala Val Ala Ser Leu Leu Pro Ser Pro
 -15 -10 -5
 Gly Asn Ser Glu Leu Pro Val Gln Ala Leu Gly Arg Arg Gly Gly Arg
 1 5 10 15
 Asp Trp Ala Arg Asn Glu Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg
 20 25 30
 Leu His Cys Ser Gly Arg Gly Arg Leu Glu Glu Pro Val Pro Pro Asn
 35 40 45
 His Leu Pro Val Gly Leu Ser Val Arg Gly Ser Gln Val Leu Ser Ser
 50 55 60
 Ala Gly Pro Arg Arg Cys Arg Leu Thr Gly Thr Arg Asn Pro Val Arg
 65 70 75
 Gly Pro Arg Arg Val Glu Gln Ile Ala Arg Gly Gly Pro Glu Ala Arg
 80 85 90 95
 Arg Gln Ala Gly Asp Ser Cys
 100

<210> 320
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 320
 Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His
 -35 -30 -25
 Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala Leu Cys
 -20 -15 -10
 Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg Tyr Leu
 -5 1 5
 Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn Gly Val
 10 15 20 25
 Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu Phe Asp
 30 35 40
 Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr Arg
 45 50 55

<210> 321
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 321
 Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe Ser Leu Met Val Thr
 -35 -30 -25
 Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe Cys Val Cys Val Ile
 -20 -15 -10
 Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly Tyr Ala Phe His Phe
 -5 1 5
 Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser Ala His Arg Ala Leu
 10 15 20 25
 Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro Ala Leu Cys
 30 35 40
 Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu Ser Tyr Leu
 45 50 55
 Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys Val Thr Gly
 60 65 70
 Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser Ala His Pro
 75 80 85
 Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser Lys Glu Arg
 90 95 100 105
 Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala Thr Leu Leu
 110 115 120
 Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp Leu Ala Val Ala Ser
 125 130 135
 Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys Leu Phe Val Cys
 140 145 150

<210> 322
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 322

Met Pro Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp
 -40 -35 -30
 Asp Ser Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu
 -25 -20 -15 -10
 Ala Gln Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val
 -5 1 5
 Met Ser Arg Asp Gly Asn Ile Lys Asp Ser Gly Glu Asp Thr Gln Ser
 10 15 20
 Gly Thr Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser
 25 30 35
 Ser Arg Leu Thr Phe Gln Arg Arg Phe
 40 45

<210> 323

<211> 70

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -38...-1

<400> 323

Met Ser Ser Pro Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu
 -35 -30 -25
 Thr Thr Ala Ile Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe
 -20 -15 -10
 Phe Thr Pro Leu Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys
 -5 1 5 10
 Val Thr Lys Asp Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys
 15 20 25
 Glu Ala Thr Trp Leu Pro
 30

<210> 324

<211> 168

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -25...-1

<400> 324

Met Arg Gly Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu
 -25 -20 -15 -10
 Leu Val Val Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp
 -5 1 5
 Glu Arg Leu Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu
 10 15 20
 Val Leu Ala Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met
 25 30 35
 Leu Ala Ala Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe
 40 45 50 55
 Leu Ile Ala Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala
 60 65 70

Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
75 80 85
Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala
90 95 100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
105 110 115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
120 125 130 135
Cys Trp Ile Pro Ser Pro Pro Ala
140

<210> 325
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 325
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15 -10 -5 1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
5 10 15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
20 25 30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
35 40 45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
50 55 60 65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
70 75 80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
85 90 95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
100 105 110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
115 120 125
Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
130 135 140 145
Lys Gly Arg Arg Arg Gln
150

<210> 326
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 326
Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
-15 -10 -5 1
Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
5 10 15

Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
 20 25 30
 Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr
 35 40 45
 Thr Arg Arg Pro Ala Phe Pro Val Ile His Leu Glu Asp Ile Thr Leu
 50 55 60 65
 Asp Tyr Ser Asp Val Asp Ser Phe Thr Gly Ser Pro Val Ser Met Leu
 70 75 80
 Asn Asp Leu Ile Thr Phe Asp Thr Thr Lys Phe Gly Glu Thr Met Thr
 85 90 95
 Pro Glu Thr Asn Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Ala Thr
 100 105 110
 Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr
 115 120 125
 Met Pro Pro Pro Ser Gln Thr Ala Leu Thr His Asn
 130 135 140

<210> 327
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 327
 Met Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu
 -30 -25 -20
 Ser Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys
 -15 -10 -5
 Leu Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp
 1 5 10 15
 Ala Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr
 20 25 30
 Asn Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln
 35 40 45
 Cys Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro
 50 55 60
 Cys Cys Cys Asp Ile Asn Glu Gly Leu
 65 70

<210> 328
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 328
 Met Ser Asp Glu Asp Glu Ser Ser Asp Tyr Leu Cys Leu Ser Ile Leu
 -25 -20 -15
 Gly Leu Phe Cys Cys Leu Pro Leu Ala Ile Pro Ala Val Ile Phe Ser
 -10 -5 1 5
 Cys Leu Thr Lys Asn Tyr Asn Lys Ser Ser Asp Tyr Glu Leu Ala Ala
 10 15 20

Lys Thr Ser Lys Gln Ala Tyr Tyr Trp Ala Ile Ala Ser Ile Thr Val
 25 30 35
 Gly Ile Leu Gly Thr Ile Leu Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg
 40 45 50
 Leu

<210> 329
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 329
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly Ser Leu Thr
 -25 -20 -15
 Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val Phe Pro Gln
 -10 -5 1 5
 Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys Ile Ser Leu
 10 15 20
 Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln Gly Asp Leu
 25 30 35
 Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe Ser Ile Ile
 40 45 50
 Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val Gly Arg
 55 60 65

<210> 330
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 330
 Met Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His
 -20 -15 -10 -5
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly
 1 5 10
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys
 15 20 25
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser
 30 35 40
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn
 45 50 55 60
 Thr Val Arg Thr

<210> 331
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -32...-1

<400> 331

Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro
 -30 -25 -20
 Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala
 -15 -10 -5
 Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe
 1 5 10 15
 Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys
 20 25 30
 Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro
 35 40 45
 Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met
 50 55 60
 Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp
 65 70 75 80
 Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
 85 90

<210> 332

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -46...-1

<400> 332

Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp
 -45 -40 -35
 Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile
 -30 -25 -20 -15
 Thr Ala Val Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu
 -10 -5 1
 Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu Glu
 5 10 15

<210> 333

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 333

Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
 -20 -15 -10
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
 -5 1 5
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys
 10 15 20 25
 Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe
 30 35 40
 Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys

45 50 55
 Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu
 60 65 70
 Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr
 75 80 85
 Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His Pro
 90 95 100 105
 Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu
 110 115 120
 Glu Gly Ala Arg Arg Tyr
 125

<210> 334
 <211> 198
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 334
 Met Leu Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp
 -10 -5 1
 Ala Gly Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg
 5 10 15
 Val Cys Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala
 20 25 30 35
 Ala Ser Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val
 40 45 50
 Pro Arg Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg
 55 60 65
 Cys Phe Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro
 70 75 80
 Pro Gln Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu
 85 90 95
 Gln Gly Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn
 100 105 110 115
 Val Leu Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys
 120 125 130
 Leu Val Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg
 135 140 145
 Leu Arg Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp
 150 155 160
 Leu Lys Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys
 165 170 175
 Ile Tyr Leu Arg Gly Lys
 180 185

<210> 335
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

09676997 060804

<400> 335

Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala Leu Glu
 -20 -15 -10
 Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly Leu Val
 -5 1 5
 Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe Leu Met
 10 15 20
 Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu Ser Asp
 25 30 35 40
 Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val Leu Ile
 45 50 55
 Ile Leu Glu Val Leu Gln Phe Gln
 60

<210> 336

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45...-1

<400> 336

Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe
 -45 -40 -35 -30
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln
 -25 -20 -15
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro
 -10 -5 1
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly
 5 10 15
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala
 20 25 30 35
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro
 40 45 50
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro
 55 60 65
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys
 70 75 80
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu
 85 90 95
 Asp Val Phe Arg Met Thr
 100 105

<210> 337

<211> 142

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 337

Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr

		1				5				10				
Cys	Phe	Val	Tyr	Gly	Gln	Asp	Trp	Ala	Pro	Thr	Ala	Gly	Leu	Glu
15						20					25			
Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala
30					35					40				45
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro
				50					55				60	
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe
			65					70					75	
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser
		80					85					90		Pro
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr
	95					100					105			Ser
Lys	Leu	Gln	Lys	Phe	Thr	Arg	Ser	Ala	Ser	Cys	Ser	Thr	His	
110					115					120				

<210> 338
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<220>
 <221> UNSURE
 <222> 21
 <223> Xaa = Ala,Pro

Thr	Ser	Glu	Glu	Arg	Thr	Ala	Met	Lys	Arg	Glu	Gly	Gly	Ala	Ala
		-25					-20					-15		His
Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn
	-10					-5				1				5
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg
				10					15				20	Xaa
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser
		25					30					35		Ser
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly
		40					45					50		Ser
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp
	55					60					65			Arg
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg
70					75					80				85

<210> 339
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 339
 Met Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro
 -30 -25 -20

Ala Cys Lys
115

<210> 342
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39...-1

<400> 342
Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
10 15 20 25
Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
Leu Leu Leu
 60

<210> 343
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43...-1

<400> 343
Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile
 -40 -35 -30
Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly
 -25 -20 -15
Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val
 -10 -5 1 5
Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu
 10 15 20
Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser
 25 30 35
Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys
 40 45 50
Arg Tyr
 55

<210> 344
<211> 217
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<220>
 <221> UNSURE
 <222> 185
 <223> Xaa = Phe,Val

<400> 344
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser
 1 5 10
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala
 15 20 25
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His
 30 35 40 45
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu
 50 55 60
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu
 65 70 75
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp
 80 85 90
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser
 95 100 105
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly
 110 115 120 125
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His
 130 135 140
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu
 145 150 155
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser
 160 165 170
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys
 175 180 185
 Phe Gly Gly Asp Arg Leu Thr Leu His
 190 195

<210> 345
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 345
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 -20 -15 -10 -5
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 1 5 10
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 15 20 25
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 30 35 40
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

45 50 55 60
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 65 70 75
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 80 85 90
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 95 100 105
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
 110 115 120
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 125 130 135 140
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 145 150 155
 Asp Arg His Lys Met Leu Ser
 160

<210> 346
 <211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 346
 Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
 -10 -5 1
 Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
 5 10 15
 Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
 20 25 30 35
 Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr
 40 45 50
 Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg
 55 60 65
 Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
 70 75 80
 Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
 85 90 95
 Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile
 100 105 110 115
 Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly
 120 125 130
 Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
 135 140 145
 Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly
 150 155 160
 Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn
 165 170 175
 Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
 180 185 190 195
 Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg
 200 205 210
 Glu Ser Val Asn Tyr Leu Val Ser Gln Gln Asn Met Leu Leu Ile Pro
 215 220 225
 Thr Ser Phe Ser Pro Leu Lys
 230

<210> 347
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL .
 <222> -47...-1

<400> 347
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro
 -45 -40 -35
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp
 -30 -25 -20
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn
 -15 -10 -5 1
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr
 5 10 15
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp
 20 25 30
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu
 35 40 45
 Gly Leu Ala Phe Gln Cys Arg Phe
 50 55

<210> 348
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 348
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val
 -20 -15 -10
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg
 -5 1 5 10
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala
 15 20 25
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn
 30 35 40
 Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu
 45 50 55
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser
 60 65 70 75
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln
 80 85 90
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
 95 100

<210> 349
 <211> 302
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 349

Met	Ala	Pro	Asn	Ser	Ile	Thr	Leu	Leu	Gly	Leu	Ala	Val	Asn	Val	Val
			-15					-10					-5		
Thr	Thr	Leu	Val	Leu	Ile	Ser	Tyr	Cys	Pro	Thr	Ala	Thr	Glu	Glu	Ala
		1				5					10				
Pro	Tyr	Trp	Thr	Tyr	Leu	Leu	Cys	Ala	Leu	Gly	Leu	Phe	Ile	Tyr	Gln
15					20					25					30
Ser	Leu	Asp	Ala	Ile	Asp	Gly	Lys	Gln	Ala	Arg	Arg	Thr	Asn	Ser	Cys
				35					40					45	
Ser	Pro	Leu	Gly	Glu	Leu	Phe	Asp	His	Gly	Cys	Asp	Ser	Leu	Ser	Thr
			50					55					60		
Val	Phe	Met	Ala	Val	Gly	Ala	Ser	Ile	Ala	Ala	Arg	Leu	Gly	Thr	Tyr
		65					70					75			
Pro	Asp	Trp	Phe	Phe	Phe	Cys	Ser	Phe	Ile	Gly	Met	Phe	Val	Phe	Tyr
		80					85					90			
Cys	Ala	His	Trp	Gln	Thr	Tyr	Val	Ser	Gly	Met	Leu	Arg	Phe	Gly	Lys
95					100					105					110
Val	Asp	Val	Thr	Glu	Ile	Gln	Ile	Ala	Leu	Val	Ile	Val	Phe	Val	Leu
				115					120					125	
Ser	Ala	Phe	Gly	Gly	Ala	Thr	Met	Trp	Asp	Tyr	Thr	Gly	Thr	Ser	Val
			130					135					140		
Leu	Ser	Pro	Gly	Leu	His	Ile	Gly	Leu	Ile	Ile	Ile	Leu	Ala	Ile	Met
		145					150					155			
Ile	Tyr	Lys	Lys	Ser	Ala	Thr	Asp	Val	Phe	Glu	Lys	His	Pro	Cys	Leu
		160				165					170				
Tyr	Ile	Leu	Met	Phe	Gly	Cys	Val	Phe	Ala	Lys	Val	Ser	Gln	Lys	Leu
175					180					185					190
Val	Val	Ala	His	Met	Thr	Lys	Ser	Glu	Leu	Tyr	Leu	Gln	Asp	Thr	Val
				195					200					205	
Phe	Leu	Gly	Pro	Gly	Leu	Leu	Phe	Leu	Asp	Gln	Tyr	Phe	Asn	Asn	Phe
			210					215					220		
Ile	Asp	Glu	Tyr	Val	Val	Leu	Trp	Met	Ala	Met	Val	Ile	Ser	Ser	Phe
		225					230					235			
Asp	Met	Val	Ile	Tyr	Phe	Ser	Ala	Leu	Cys	Leu	Gln	Ile	Ser	Arg	His
		240				245					250				
Leu	His	Leu	Asn	Ile	Phe	Lys	Thr	Ala	Cys	His	Gln	Ala	Pro	Glu	Gln
255					260					265					270
Val	Gln	Val	Leu	Ser	Ser	Lys	Ser	His	Gln	Asn	Asn	Met	Asp		
				275					280						

<210> 350
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 350

Met	Ile	Leu	Val	Thr	Val	Pro	Gly	Val	Cys	Pro	Ala	Gln	Cys	Cys	Trp
				-10					-5					1	
Ala	Glu	Gln	Arg	Gly	Arg	Gly	Ser	Gly	Met	Tyr	Phe	Ile	Asp	Lys	Trp
		5					10					15			

Ala Arg Pro Ser Trp Val Pro His Trp Leu Asn Asp Leu Phe Ile Val
 20 25 30
 Lys Ser Gly Tyr Leu Val Cys Ile Arg Thr Thr Val Ile Arg Gln Gly
 35 40 45 50
 Ile Val Arg Ile Gly Arg Asn Lys Ile Ser Glu Ser Gly Arg Ser Ala
 55 60 65
 Leu Tyr Thr Ile Ala Lys Asn Lys Met Val Ile Phe Lys Val Pro Asp
 70 75 80
 Cys Met His Leu Asn Ala Asp Tyr Phe Gly Val
 85 90

<210> 351
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 351
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
 115 120 125
 Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
 130 135 140
 Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
 145 150 155
 Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
 160 165 170
 Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
 175 180 185 190
 Ala Ser Glu Lys Lys
 195

<210> 352
 <211> 206
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -34...-1

<400> 352

Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp	Ser
			-30						-25					-20	
Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Leu	Ala
		-15					-10						-5		
Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala	Leu	Glu	Tyr
	1				5						10				
Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu	Pro	Arg	Thr	Phe
15					20					25					30
Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala	Val	Ile	Met	Ala	Val
				35					40					45	
Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu	Glu	Ala	Ala	Asp	Leu	Ser
			50					55					60		
Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu	Gly	Val	Pro	Leu	Tyr	Ala	Val
	65						70					75			
Val	Lys	Glu	His	Ile	Arg	Thr	Glu	Val	Lys	Asp	Phe	Gln	Pro	Tyr	Phe
	80					85					90				
Lys	Gly	Glu	Ile	Phe	Leu	Asp	Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln
95					100					105					110
Arg	Arg	Lys	Met	Met	Phe	Met	Gly	Phe	Ile	Arg	Leu	Gly	Val	Trp	Tyr
				115					120					125	
Asn	Phe	Phe	Arg	Ala	Trp	Asn	Gly	Gly	Phe	Ser	Gly	Asn	Leu	Glu	Gly
			130					135					140		
Glu	Gly	Phe	Ile	Leu	Gly	Gly	Val	Phe	Val	Val	Gly	Ser	Gly	Ser	Arg
		145				150					155				
Ala	Phe	Phe	Leu	Ser	Thr	Glu	Lys	Lys	Asn	Leu	Glu	Thr	Lys		
	160					165					170				

<210> 353
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44...-1

<400> 353

Met	Ala	Ala	Glu	Gly	Trp	Ile	Trp	Arg	Trp	Gly	Trp	Gly	Arg	Arg	Cys
			-40						-35					-30	
Leu	Gly	Arg	Pro	Gly	Leu	Leu	Gly	Pro	Gly	Pro	Gly	Pro	Thr	Thr	Pro
		-25						-20					-15		
Leu	Phe	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Val	Thr	Ala	Asp	Ile	Thr	Asp
		-10					-5					1			
Gly	Asn	Ile	Glu	His	Leu	Lys	Arg	Glu	His	Ser	Leu	Ile	Lys	Pro	Tyr
5					10					15					20
Gln	Gly	Val	Gly	Ser	Ser	Ser	Pro	Ser	Gly	Thr	Ser	Arg	Ala	Ala	Leu
				25					30					35	
Cys	Ser	Arg	Ala	Ser	Thr	Tyr	Val								
				40											

<210> 354
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32...-1

<400> 354
Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg
-30 -25 -20
His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser
-15 -10 -5
Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu
1 5 10 15
Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser
20 25 30
Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp
35 40 45
Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala
50 55 60
Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile
65 70 75 80
Asp Gly Lys Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr
85 90 95
Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp
100 105 110
Arg Leu Lys Gln Gly Lys Phe
115

<210> 355
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 355
Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala
-15 -10 -5
Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly
1 5 10 15
His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser
20 25 30
Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr
35 40 45
Leu

<210> 356
<211> 189
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<220>
<221> UNSURE

<222> 41
<223> Xaa = Ala,Gly

<400> 356
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
-20 -15 -10
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
-5 1 5
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
10 15 20
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
25 30 35 40
Xaa Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
45 50 55
Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
60 65 70
Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
75 80 85
Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
90 95 100
Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
105 110 115 120
Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
125 130 135
His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
140 145 150
Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
155 160 165

<210> 357
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47...-1

<400> 357
Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro Phe Ala Phe Glu
-45 -40 -35
Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser Leu Ser Asp Pro
-30 -25 -20
Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met Ala Leu Cys Ala
-15 -10 -5 1
Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys Lys Leu Ile Leu
5 10 15
Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile Val Ala Leu Leu
20 25 30
Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser Lys Glu Gln Gln
35 40 45
Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu Cys Gly Gly Val
50 55 60 65
Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser Ser Asp Ser Ser
70 75 80
Ala Ser Val Ser Arg Val Asp Gly Thr Gly Thr Arg His His Ala
85 90 95
Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser Pro Tyr Trp Pro

100 105 110
 Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
 115 120 125
 Lys Val Leu Gly Leu Pro Ala
 130 135

<210> 358
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 358
 Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
 Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
 Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
 20 25 30
 Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
 35 40 45 50
 Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
 55 60 65
 Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
 70 75 80
 Val Thr Lys Lys Trp Ser
 85

<210> 359
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 359
 Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala Ile Tyr Ile Leu Thr
 -25 -20 -15
 Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu Trp Ser Trp Ile Cys
 -10 -5 1
 Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn
 5 10 15
 Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu
 20 25 30 35
 Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu Glu Val Gly Cys Gly
 40 45 50
 Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
 55 60 65
 Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala
 70 75 80
 Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu
 85 90 95
 Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Val Cys Thr

100 105 110 115
 Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val
 120 125 130
 Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val
 135 140 145
 Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp
 150 155 160
 Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser
 165 170 175
 Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His
 180 185 190 195
 Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg Pro His Ile Tyr Gly
 200 205 210
 Tyr Ala Val Lys
 215

<210> 360
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 360
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
 -20 -15 -10
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
 -5 1 5
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys
 10 15 20 25
 Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys Cys
 30 35 40
 Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile Tyr
 45 50 55
 Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val His
 60 65 70
 Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys Gln
 75 80 85
 Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile Asn
 90 95 100 105
 Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val Ile
 110 115 120
 Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys Ile
 125 130 135
 Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg Arg
 140 145 150
 Tyr

<210> 361
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 361

Met	Ala	Leu	Cys	Ala	Leu	Thr	Arg	Ala	Leu	Pro	Ser	Leu	Asn	Leu	Ala
-20						-15					-10				
Pro	Pro	Thr	Val	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Phe	Pro	Ala	Ala	Gln
-5					1				5					10	
Met	Met	Asn	Asn	Gly	Leu	Leu	Gln	Gln	Pro	Ser	Ala	Leu	Met	Leu	Leu
		15					20					25			
Pro	Cys	Arg	Pro	Val	Leu	Thr	Ser	Val	Ala	Leu	Asn	Ala	Asn	Phe	Val
	30						35				40				
Ser	Trp	Lys	Ser	Arg	Thr	Lys	Tyr	Thr	Ile	Thr	Pro	Val	Lys	Met	Arg
	45					50					55				
Lys	Ser	Gly	Gly	Arg	Asp	His	Thr	Gly	Ala	Gly	Asn	Val	Arg	Arg	Thr
60					65					70					75
Val	Gly	Arg	Val	Ser	Asn	Val	Asp	His	Asn	Lys	Arg	Val	Ile	Gly	Lys
				80					85					90	
Ala	Gly	Arg	Asn	Arg	Trp	Leu	Gly	Lys	Arg	Pro	Asn	Ser	Gly	Arg	Trp
			95					100					105		
His	Arg	Lys	Gly	Gly	Trp	Ala	Gly	Arg	Lys	Ile	Arg	Pro	Leu	Pro	Pro
		110					115					120			
Met	Lys	Ser	Tyr	Val	Lys	Leu	Pro	Ser	Ala	Ser	Ala	Gln	Ser		
	125					130					135				

<210> 362

<211> 186

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 362

Met	Ala	Thr	Ala	Ser	Pro	Ser	Val	Phe	Leu	Leu	Met	Val	Asn	Gly	Gln
				-15					-10					-5	
Val	Glu	Ser	Ala	Gln	Phe	Pro	Glu	Tyr	Asp	Asp	Leu	Tyr	Cys	Lys	Tyr
			1				5					10			
Cys	Phe	Val	Tyr	Gly	Gln	Asp	Trp	Ala	Pro	Thr	Ala	Gly	Leu	Glu	Glu
	15				20						25				
Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu
30					35					40					45
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr
				50					55					60	
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly
			65					70					75		
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro
	80						85					90			
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser
	95					100					105				
Lys	Leu	Gln	Lys	Phe	Thr	Ser	Trp	Phe	Met	Gly	Arg	Arg	Pro	Glu	Tyr
110					115					120					125
Thr	Asp	Pro	Lys	Val	Val	Ala	Gln	Gly	Glu	Gly	Arg	Glu	Ala	Ile	Thr
				130					135					140	
Ala	Pro	Arg	Lys	Ala	Val	Phe	Ser	Val	His	Gly	Leu	Thr	Ser	Pro	Arg
			145					150					155		
Ala	Leu	Ala	Leu	Val	His	Ile	Lys	Gly	Thr						
	160						165								

[illegible][illegible][illegible]

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible][illegible][illegible]

<220>
<221> SIGNAL
<222> -26...-1

<400> 365
Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln Gly Phe Cys Gly
-25 -20 -15
Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe Phe Lys Lys Asn
-10 -5 1 5
Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu Gly Gly Met Gly
10 15 20
Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp Leu Phe Ala Trp
25 30 35
Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly Phe Glu Asn Met
40 45 50
Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro Ser Thr
55 60 65

<210> 366
<211> 140
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40...-1

<400> 366
Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
-40 -35 -30 -25
Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
-20 -15 -10
Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
-5 1 5
Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
10 15 20
Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
25 30 35 40
Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
45 50 55
Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
60 65 70
Leu Ala Phe Thr Ser Val Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu
75 80 85
Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
90 95 100

<210> 367
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35...-1

<400> 367

Met Asp Pro Gly Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met
 -35 -30 -25 -20
 Ala Val Leu Phe Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro
 -15 -10 -5
 Val Trp Gly Trp Ser Pro Gly
 1

<210> 368
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 368
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
 -40 -35 -30
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
 -25 -20 -15 -10
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
 -5 1 5
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
 10 15 20
 Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
 25 30 35

<210> 369
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 369
 Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
 -40 -35 -30 -25
 Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
 -20 -15 -10
 Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
 -5 1 5
 Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
 10 15 20
 Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
 25 30 35 40
 Lys Ser Lys

<210> 370
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 370

Met	Ala	Val	Leu	Ala	Gly	Ser	Leu	Leu	Gly	Pro	Thr	Ser	Arg	Ser	Ala	
-15					-10					-5					1	
Ala	Leu	Leu	Gly	Gly	Arg	Trp	Leu	Gln	Pro	Arg	Ala	Trp	Leu	Gly	Phe	
		5						10					15			
Pro	Asp	Ala	Trp	Gly	Leu	Pro	Thr	Pro	Gln	Gln	Ala	Arg	Gly	Lys	Ala	
	20					25						30				
Arg	Gly	Asn	Glu	Tyr	Gln	Pro	Ser	Asn	Ile	Lys	Arg	Lys	Asn	Lys	His	
	35				40						45					
Gly	Trp	Val	Arg	Arg	Leu	Ser	Thr	Pro	Ala	Gly	Val	Gln	Val	Ile	Leu	
50					55					60					65	
Arg	Arg	Met	Leu	Lys	Gly	Arg	Lys	Ser	Leu	Ser	His					
			70						75							

<210> 371

<211> 279

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 371

Met	Ala	Ala	Pro	Val	Arg	Arg	Thr	Leu	Leu	Gly	Val	Ala	Gly	Gly	Trp	
	-40						-35					-30				
Arg	Arg	Phe	Glu	Arg	Leu	Trp	Ala	Gly	Ser	Leu	Ser	Ser	Arg	Ser	Leu	
	-25					-20					-15					
Ala	Leu	Ala	Ala	Ala	Pro	Ser	Ser	Asn	Gly	Ser	Pro	Trp	Arg	Leu	Leu	
-10					-5				1				5			
Gly	Ala	Leu	Cys	Leu	Gln	Arg	Pro	Pro	Val	Val	Ser	Lys	Pro	Leu	Thr	
		10					15					20				
Pro	Leu	Gln	Glu	Glu	Met	Ala	Ser	Leu	Leu	Gln	Gln	Ile	Glu	Ile	Glu	
	25					30					35					
Arg	Ser	Leu	Tyr	Ser	Asp	His	Glu	Leu	Arg	Ala	Leu	Asp	Glu	Asn	Gln	
	40				45					50						
Arg	Leu	Ala	Lys	Lys	Lys	Ala	Asp	Leu	His	Asp	Glu	Glu	Asp	Glu	Gln	
55					60					65					70	
Asp	Ile	Leu	Leu	Ala	Gln	Asp	Leu	Glu	Asp	Met	Trp	Glu	Gln	Lys	Phe	
			75					80						85		
Leu	Gln	Phe	Lys	Leu	Gly	Ala	Arg	Ile	Thr	Glu	Ala	Asp	Glu	Lys	Asn	
		90					95					100				
Asp	Arg	Thr	Ser	Leu	Asn	Arg	Asn	Leu	Asp	Arg	Asn	Leu	Val	Leu	Leu	
	105					110					115					
Val	Arg	Glu	Lys	Phe	Gly	Asp	Gln	Asp	Val	Trp	Ile	Leu	Pro	Gln	Ala	
	120				125						130					
Glu	Trp	Gln	Pro	Gly	Glu	Thr	Leu	Arg	Gly	Thr	Ala	Glu	Arg	Thr	Leu	
135					140					145					150	
Ala	Thr	Leu	Ser	Glu	Asn	Asn	Met	Glu	Ala	Lys	Phe	Leu	Gly	Asn	Ala	
			155					160						165		
Pro	Cys	Gly	His	Tyr	Thr	Phe	Lys	Phe	Pro	Gln	Ala	Met	Arg	Thr	Glu	
			170				175					180				
Ser	Asn	Leu	Gly	Ala	Lys	Val	Phe	Phe	Phe	Lys	Ala	Leu	Leu	Leu	Thr	
	185					190						195				
Gly	Asp	Phe	Ser	Gln	Ala	Gly	Asn	Lys	Gly	His	His	Val	Trp	Val	Ile	
	200				205					210						
Lys	Asp	Glu	Leu	Gly	Asp	Tyr	Leu	Lys	Pro	Lys	Tyr	Leu	Ala	Gln	Val	

230

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<220>
<221> SIGNAL
<222> -31...-1
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<220>
<221> SIGNAL
<222> -42..-1
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340

25 30 35
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala
 40 45 50
 Cys Thr His Arg Asp
 55

<210> 374
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 374
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser
 -20 -15 -10 -5
 Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu
 1 5 10
 Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln
 15 20 25
 Gln Pro Cys Lys Ser Gly Gly Gly Val Gly Glu Pro Asn Ala Gln
 30 35 40
 Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser
 45 50 55 60
 His Gly Gln Ala Phe
 65

<210> 375
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 375
 Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val
 -25 -20 -15
 Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys
 -10 -5 1
 Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val
 5 10 15 20
 Met Leu Val Ala Pro Phe Arg Gln Ser Ser Ser Leu Ser Arg Thr Phe
 25 30 35
 Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg
 40 45 50
 Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly
 55 60

<210> 376
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -33...-1

<220>
<221> UNSURE
<222> 47
<223> Xaa = Ala,Pro,Ser,Thr

<400> 376
Met Ala Gln Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu
-30 -25 -20
Ala Pro Thr Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser
-15 -10 -5
Ser Ala Pro Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu
1 5 10 15
Leu Leu Leu Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Ala
20 25 30
Pro Ala Arg Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa
35 40 45
Gly Pro Leu Ile Pro Gly Gln Cys Pro
50 55

<210> 377
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 377
Met Asn Arg Val Leu Cys Ala Pro Ala Ala Gly Ala Val Arg Ala Leu
-15 -10 -5 1
Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu His Pro Leu Pro Gly Ser
5 10 15
Arg Asp Arg Ala His Pro Ala Ala Glu Glu Glu Asp Asp Pro Asp Arg
20 25 30
Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn Pro His Arg Trp Ser Val
35 40 45
Gly His Thr Met Gly Lys Gly His Gln Arg Pro Trp Trp Lys Val Leu
50 55 60 65
Pro Leu Ser Cys Phe Leu Val Ala Leu Ile Ile Trp Cys Tyr Leu Arg
70 75 80
Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg Gln Val Trp Gly Glu Val
85 90 95
Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro Glu Thr Pro Ala Ala Tyr
100 105 110
Arg Ala Arg Thr
115

<210> 378
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -14...-1

<220>

<221> UNSURE

<222> 50

<223> Xaa = Ala,Gly

<220>

<221> UNSURE

<222> 51

<223> Xaa = Leu,Met,Val

<400> 378

Met	Phe	Leu	Thr	Ala	Leu	Leu	Trp	Arg	Gly	Arg	Ile	Pro	Gly	Arg	Gln
				-10					-5					1	
Trp	Ile	Gly	Lys	His	Arg	Arg	Pro	Arg	Phe	Val	Ser	Leu	Arg	Ala	Lys
		5					10					15			
Gln	Asn	Met	Ile	Arg	Arg	Leu	Glu	Ile	Asp	Ala	Glu	Asn	His	Tyr	Trp
	20					25					30				
Leu	Ser	Met	Pro	Tyr	Met	Thr	Arg	Glu	Gln	Glu	Arg	Gly	His	Ala	Xaa
35					40					45					50
Xaa	Arg	Arg	Arg	Glu	Ala	Phe	Glu	Ala	Ile	Lys	Ala	Ala	Ala	Thr	Ser
				55					60					65	
Lys	Phe	Pro	Pro	His	Arg	Phe	Ile	Ala	Asp	Gln	Leu	Asp	His	Leu	Asn
			70					75						80	
Val	Thr	Lys	Lys	Trp	Ser										
			85												

<210> 379

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 379

Met	Gly	Ile	Lys	Thr	Ala	Leu	Pro	Ala	Ala	Glu	Leu	Gly	Leu	Tyr	Ser
				-20					-15					-10	
Leu	Val	Leu	Ser	Gly	Ala	Leu	Ala	Tyr	Ala	Gly	Arg	Gly	Leu	Leu	Glu
			-5					1				5			
Ala	Ser	Gln	Asp	Gly	Ala	His	Arg	Lys	Ala	Phe	Arg	Glu	Ser	Val	Arg
	10					15				20					
Pro	Gly	Trp	Glu	Tyr	Ile	Gly	Arg	Lys	Met	Asp	Val	Ala	Asp	Phe	Glu
25					30					35					40
Trp	Val	Met	Trp	Phe	Thr	Ser	Phe	Arg	Asn	Val	Ile	Ile	Phe	Ala	Leu
				45					50					55	
Ser	Gly	His	Val	Leu	Phe	Ala	Lys	Leu	Cys	Thr	Met	Val	Ala	Pro	Lys
			60					65				70			
Leu	Arg	Ser	Trp	Met	Tyr	Ala	Val	Tyr	Gly	Ala	Leu	Ala	Val	Met	Gly
		75					80					85			
Thr	Met	Gly	Pro	Trp	Tyr	Leu	Leu	Leu	Leu	Gly	His	Cys	Val	Gly	
	90					95				100					
Leu	Tyr	Val	Ala	Ser	Leu	Leu	Gly	Gln	Pro	Trp	Leu	Cys	Leu	Gly	Leu
105					110					115					120
Gly	Leu	Ala	Ser	Leu	Ala	Ser	Phe	Lys	Met	Asp	Pro	Leu	Ile	Ser	Trp
				125					130					135	

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Gln	Ser	Gly	Phe	Val	Thr	Gly	Thr	Phe	Asp	Leu	Gln	Glu	Val	Leu	Phe
			140					145					150		
His	Gly	Gly	Ser	Ser	Phe	Thr	Val	Leu	Arg	Cys	Thr	Ser	Phe	Ala	Leu
		155					160					165			
Glu	Ser	Cys	Ala	His	Pro	Asp	Arg	His	Tyr	Ser	Leu	Ala	Asp	Leu	Leu
	170					175					180				
Lys	Tyr	Ser	Phe	Tyr	Leu	Pro	Phe	Phe	Phe	Phe	Gly	Pro	Ile	Met	Thr
185					190					195					200
Phe	Asp	Arg	Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg
			205						210					215	
Glu	Gly	Glu	Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val
			220					225					230		
Ala	Ile	Met	Ala	Val	Asp	Ile	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr	
		235					240				245				
Ile	Pro	Ser	Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu
	250					255					260				
Ala	Gly	Leu	Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala
265					270					275					280
Val	Leu	Phe	Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp
			285						290					295	
Pro	Pro	Gln	Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu
			300					305					310		
Thr	His	Phe	Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr
		315					320					325			
Asn	His	Ile	Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala
	330					335					340				
Thr	Val	Ala	Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp
345					350					355					360
Ile	Val	Tyr	Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu
			365						370					375	
Leu	Trp	Met	Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu
		380						385					390		
Ala	Ser	Leu	Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly
		395					400					405			
Ala	Met	Asn	Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn
	410					415					420				
Ser	Leu	Lys	Phe	Thr	Glu	Leu	Val	Ala	Arg	Arg	Leu	Leu	Leu	Thr	Gly
425					430					435					440
Phe	Pro	Gln	Thr	Thr	Leu	Ser	Ile	Leu	Phe	Val	Thr	Tyr	Cys	Gly	Val
			445						450					455	
Gln	Leu	Val	Lys	Glu	Arg	Glu	Arg	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Gln
		460						465					470		
Lys	Gln	Asp	Lys	Glu	Lys	Pro	Glu								
	475						480								

<210> 380

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 380

Met	Val	Thr	Phe	Pro	Asp	Val	Pro	Leu	Gly	Ile	Phe	Leu	Phe	Cys	Val
-25						-20					-15				

Cys	Val	Ile	Ala	Ile	Gly	Val	Val	Gln	Ala	Leu	Ile	Val	Gly	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<210> 383
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 383
 Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
 -45 -40 -35
 Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
 -30 -25 -20
 Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
 -15 -10 -5
 Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys
 1 5 10 15
 Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
 20 25 30
 Arg Ser Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
 35 40 45

<210> 384
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 384
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
 80 85 90
 Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala Pro
 95 100 105
 Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met Ala
 110 115 120
 Ser Met Glu Ser Pro Gln
 125 130

<210> 385
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 385
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
1 5 10 15
Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
20 25 30
Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr
35 40 45
Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro
50 55 60
Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln
65 70 75 80
Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala
85 90 95
Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr
100 105 110
Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met
115 120 125
Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln
130 135 140
Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser
145 150 155 160
Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys
165 170 175
Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe
180 185 190
Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu
195 200 205
Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val
210 215 220
Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser
225 230 235 240
Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly
245 250 255
Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala
260 265 270
Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly
275 280 285
Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu
290 295 300
Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys
305 310 315 320
Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly
325 330 335
Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
340 345 350
Gly Val

<210> 386
<211> 207
<212> PRT
<213> Homo sapiens

<400> 386
Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala
1 5 10 15
Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe
20 25 30

Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp
 35 40 45
 Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val
 50 55 60
 Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp
 65 70 75 80
 Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val Thr Val Lys Arg
 85 90 95
 Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp Met Ser Arg Asp
 100 105 110
 Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe Thr Tyr Ala Gln
 115 120 125
 Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala Pro Val Glu Gly
 130 135 140
 Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu Tyr Glu Ala Gln
 145 150 155 160
 Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val Val His Thr Leu
 165 170 175
 Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe Ala Leu Trp Asp
 180 185 190
 Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro Glu Gly Leu
 195 200 205

<210> 387

<211> 210

<212> PRT

<213> Homo sapiens

<400> 387

Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
 1 5 10 15
 Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
 20 25 30
 Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
 35 40 45
 Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
 50 55 60
 Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
 65 70 75 80
 Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
 85 90 95
 Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
 100 105 110
 Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
 115 120 125
 Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
 130 135 140
 Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
 145 150 155 160
 Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
 165 170 175
 Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
 180 185 190
 Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
 195 200 205
 Leu Gln
 210

<210> 388
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 388
 Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
 1 5 10 15
 Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
 20 25 30
 Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
 35 40 45
 Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
 50 55 60
 Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu
 65 70 75 80
 Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys
 85 90 95
 Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Gln Phe Tyr Ser
 100 105 110
 Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr
 115 120 125
 Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser
 130 135 140
 Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala
 145 150 155 160
 Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser
 165 170 175
 Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala
 180 185 190
 Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp
 195 200 205
 Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr
 210 215 220
 Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val
 225 230 235 240
 Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala
 245 250 255
 Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His
 260 265 270
 Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu
 275 280 285
 Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr
 290 295 300
 Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro
 305 310 315 320
 Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile
 325 330 335
 Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe
 340 345 350
 Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu
 355 360 365
 Lys Met Ser Gly Arg Lys His
 370 375

<210> 389
 <211> 509
 <212> PRT

<213> Homo sapiens

<400> 389

Met	Ala	Ala	Ile	Gly	Val	His	Leu	Gly	Cys	Thr	Ser	Ala	Cys	Val	Ala	
1				5					10					15		
Val	Tyr	Lys	Asp	Gly	Arg	Ala	Gly	Val	Val	Ala	Asn	Asp	Ala	Gly	Asp	
			20					25					30			
Arg	Val	Thr	Pro	Ala	Val	Val	Ala	Tyr	Ser	Glu	Asn	Glu	Glu	Ile	Val	
			35				40					45				
Gly	Leu	Ala	Ala	Lys	Gln	Ser	Arg	Ile	Arg	Asn	Ile	Ser	Asn	Thr	Val	
	50					55				60						
Met	Lys	Val	Lys	Gln	Ile	Leu	Gly	Arg	Ser	Ser	Ser	Asp	Pro	Gln	Ala	
65					70					75					80	
Gln	Lys	Tyr	Ile	Ala	Glu	Ser	Lys	Cys	Leu	Val	Ile	Glu	Lys	Asn	Gly	
				85				90						95		
Lys	Leu	Arg	Tyr	Glu	Ile	Asp	Thr	Gly	Glu	Glu	Thr	Lys	Phe	Val	Asn	
			100					105					110			
Pro	Glu	Asp	Val	Ala	Arg	Leu	Ile	Phe	Ser	Lys	Met	Lys	Glu	Thr	Ala	
			115				120						125			
His	Ser	Val	Leu	Gly	Ser	Asp	Ala	Asn	Asp	Val	Val	Ile	Thr	Val	Pro	
	130					135					140					
Phe	Asp	Phe	Gly	Glu	Lys	Gln	Lys	Asn	Ala	Leu	Gly	Glu	Ala	Ala	Arg	
145					150					155					160	
Ala	Ala	Gly	Phe	Asn	Val	Leu	Arg	Leu	Ile	His	Glu	Pro	Ser	Ala	Ala	
				165					170					175		
Leu	Leu	Ala	Tyr	Gly	Ile	Gly	Gln	Asp	Ser	Pro	Thr	Gly	Lys	Ser	Asn	
			180					185					190			
Ile	Leu	Val	Phe	Lys	Leu	Gly	Gly	Thr	Ser	Leu	Ser	Leu	Ser	Val	Met	
			195				200					205				
Glu	Val	Asn	Ser	Gly	Ile	Tyr	Arg	Val	Leu	Ser	Thr	Asn	Thr	Asp	Asp	
	210					215					220					
Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr	Leu	Ala	
225					230					235					240	
Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn	Ala	Arg	
				245					250					255		
Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His	Ser	Leu	
			260					265					270			
Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr	Glu	Gly	
		275					280					285				
Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	Leu	Cys	
	290					295					300					
Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	Leu	Asp	
305					310					315					320	
Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	Cys	Gly	
				325					330					335		
Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp	Leu	Phe	
			340					345					350			
Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	Ile	Pro	
		355					360					365				
Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	Asn	Leu	
	370					375					380					
Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	Ile	Leu	
385					390					395					400	
Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	Leu	Phe	
				405					410					415		
Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Gln	His	Thr	Leu	Gln	Ala		
			420					425				430				
Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	Asp	Gly	

435 440 445
 Lys Asn Ser Ala Lys Glu Glu Thr Lys Phe Ala Gln Val Val Leu Gln
 450 455 460
 Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu
 465 470 475 480
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu
 485 490 495
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser
 500 505

<210> 390
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 390
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His
 1 5 10 15
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu
 20 25 30
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His
 35 40 45
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu
 50 55 60
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
 65 70 75

<210> 391
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 391
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly

<210> 392
 <211> 146
 <212> PRT

<213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
1 5 10 15
Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
20 25 30
Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
35 40 45
Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
50 55 60
Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
65 70 75 80
His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
85 90 95
Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
100 105 110
Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
115 120 125
Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
130 135 140
Gly Phe
145

<210> 393

<211> 225

<212> PRT

<213> Homo sapiens

<400> 393

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1 5 10 15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
20 25 30
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
35 40 45
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
50 55 60
Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
65 70 75 80
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
85 90 95
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
100 105 110
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
115 120 125
Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
130 135 140
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
145 150 155 160
Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
165 170 175
Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
180 185 190
Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
195 200 205
Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
210 215 220

Val
225

<210> 394
<211> 114
<212> PRT
<213> Homo sapiens

<400> 394
Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met
1 5 10 15
Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile
20 25 30
Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His
35 40 45
Met Ser Phe His Tyr Thr Val Val Leu Met Phe Ser Gln Val Ile Ser
50 55 60
Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn
65 70 75 80
Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser
85 90 95
Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu
100 105 110
Gln Gly

<210> 395
<211> 367
<212> PRT
<213> Homo sapiens

<400> 395
Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
1 5 10 15
Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
20 25 30
Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
35 40 45
Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
50 55 60
Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
65 70 75 80
Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
85 90 95
Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
100 105 110
Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
115 120 125
Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
130 135 140
Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
145 150 155 160
Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
165 170 175
Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
180 185 190
Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
195 200 205
Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val

210		215		220
Ser Tyr Leu Lys Lys Ile	Leu Gly Glu Leu Ala Met Val Leu Asp Gln			
225		230		235
Ile Glu Ala Glu Leu Glu Lys Arg Lys	Leu Glu Asn Glu Gly Gln Lys			240
		245		250
Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu				255
		260		265
Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys				270
		275		280
Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg				285
		290		295
Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr				300
305		310		315
Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg				320
		325		330
Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly				335
		340		345
Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile				350
		355		360
				365

<210> 396

<211> 279

<212> PRT

<213> Homo sapiens

<400> 396

Met Pro Val Cys Ala Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly				
1	5	10	15	
Met Pro Val Cys Ala Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr				
	20	25	30	
Arg Ala Val Val Cys Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly				
	35	40	45	
Cys Thr His Met Cys Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser				
	50	55	60	
Pro Leu Ala Gly Gly Val Ile Leu Gly Val Ala Leu Trp Leu Arg His				
65	70	75	80	
Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro				
	85	90	95	
Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly				
	100	105	110	
Ala Val Met Met Phe Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln				
	115	120	125	
Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu				
	130	135	140	
Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp				
145	150	155	160	
Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln				
	165	170	175	
Ala Val Val Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr				
	180	185	190	
Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu				
	195	200	205	
Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile				
	210	215	220	
Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu				
225	230	235	240	
Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala				
	245	250	255	

Val Ile Met Ile Phe Glu Met Ile Leu Ser Met Val Leu Cys Cys Gly
 260 265 270
 Ile Arg Asn Ser Ser Val Tyr
 275

<210> 397
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Cys Leu Leu Leu Gly Ala Thr Gly Val Gly Lys Thr Leu Leu Val
 1 5 10 15
 Lys Arg Leu Gln Glu Val Ser Ser Arg Asp Gly Lys Gly Asp Leu Gly
 20 25 30
 Glu Pro Pro Pro Thr Arg Pro Thr Val Gly Thr Asn Leu Thr Asp Ile
 35 40 45
 Val Ala Gln Arg Lys Ile Thr Ile Arg Glu Leu Gly Gly Cys Met Gly
 50 55 60
 Pro Ile Trp Ser Ser Tyr Tyr Gly Asn Cys Arg Ser Leu Leu Phe Val
 65 70 75 80
 Met Asp Ala Ser Asp Pro Thr Gln Leu Ser Ala Ser Cys Val Gln Leu
 85 90 95
 Leu Gly Leu Leu Ser Ala Glu Gln Leu Ala Glu Ala Ser Val Leu Ile
 100 105 110
 Leu Phe Asn Lys Ile Asp Leu Pro Cys Tyr Met Ser Thr Glu Glu Met
 115 120 125
 Lys Ser Leu Ile Arg Leu Pro Asp Ile Ile Ala Cys Ala Lys Gln Asn
 130 135 140
 Ile Thr Thr Ala Glu Ile Ser Ala Arg Glu Gly Thr Gly Leu Ala Gly
 145 150 155 160
 Val Leu Ala Trp Leu Gln Ala Thr His Arg Ala Asn Asp
 165 170

<210> 398
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 398
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Val Leu Phe Leu Cys Asp Met Gln Glu Lys Phe Arg His Asn Ile Ala
 20 25 30
 Tyr Phe Pro Gln Ile Val Ser Val Ala Ala Arg Met Leu Lys Val Ala
 35 40 45
 Arg Leu Leu Glu Val Pro Val Met Leu Thr Glu Gln Tyr Pro Gln Gly
 50 55 60
 Leu Gly Pro Thr Val Pro Glu Leu Gly Thr Glu Gly Leu Arg Pro Leu
 65 70 75 80
 Ala Lys Thr Cys Phe Ser Met Val Pro Ala Leu Gln Gln Glu Leu Asp
 85 90 95
 Ser Arg Pro Gln Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln
 100 105 110
 Ala Cys Ile Leu Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln
 115 120 125
 Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg
 130 135 140

Thr	Ser	Ser	Leu	Thr	Asp	Thr	Asp	Val	Gln	Val	Ser	Pro	Met	Leu	Val
			100					105					110		
Ala	Gly	Val	Asn	His	Ser	Ser	Ser	Leu	Leu	Asp	Asn	Ile	Pro	Phe	Thr
		115					120					125			
Gly	Cys	Leu	Pro	Phe	His	Leu	Ser	Ser	Ser	Leu	Pro	Tyr	Leu	Cys	Leu
	130					135					140				
Leu	Gly	Ser	Pro	Phe	Lys										
145					150										

<210> 401

<211> 170

<212> PRT

<213> Homo sapiens

<400> 401

Met	Glu	Asp	Pro	Asn	Pro	Glu	Glu	Asn	Met	Lys	Gln	Gln	Asp	Ser	Pro
1				5					10					15	
Lys	Glu	Arg	Ser	Pro	Gln	Ser	Pro	Gly	Gly	Asn	Ile	Cys	His	Leu	Gly
			20					25					30		
Ala	Pro	Lys	Cys	Thr	Arg	Cys	Leu	Ile	Thr	Phe	Ala	Asp	Ser	Lys	Phe
		35					40					45			
Gln	Glu	Arg	His	Met	Lys	Arg	Glu	His	Pro	Ala	Asp	Phe	Val	Ala	Gln
	50					55					60				
Lys	Leu	Gln	Gly	Val	Leu	Phe	Ile	Cys	Phe	Thr	Cys	Ala	Arg	Ser	Phe
65					70					75					80
Pro	Ser	Ser	Lys	Ala	Leu	Ile	Thr	His	Gln	Arg	Ser	His	Gly	Pro	Ala
			85						90					95	
Ala	Lys	Pro	Thr	Leu	Pro	Val	Ala	Thr	Thr	Thr	Ala	Gln	Pro	Thr	Phe
			100					105					110		
Pro	Cys	Pro	Asp	Cys	Gly	Lys	Thr	Phe	Gly	Gln	Ala	Val	Ser	Leu	Arg
		115				120						125			
Arg	His	Arg	Gln	Met	His	Glu	Val	Arg	Ala	Pro	Pro	Gly	Thr	Phe	Ala
	130					135						140			
Cys	Thr	Glu	Cys	Gly	Gln	Asp	Phe	Ala	Gln	Glu	Ala	Gly	Leu	His	Gln
145					150					155					160
His	Tyr	Ile	Arg	His	Ala	Arg	Gly	Glu	Leu						
				165					170						

<210> 402

<211> 169

<212> PRT

<213> Homo sapiens

<400> 402

Met	Glu	Asp	Pro	Asn	Pro	Glu	Glu	Asn	Met	Lys	Gln	Gln	Asp	Ser	Pro
1				5					10					15	
Lys	Glu	Arg	Ser	Pro	Gln	Pro	Arg	Arg	Gln	His	Leu	Pro	Pro	Gly	Gly
			20					25					30		
Pro	Glu	Val	His	Pro	Leu	Pro	His	His	Leu	Arg	Arg	Phe	Gln	Val	Pro
		35					40					45			
Gly	Ala	Ser	His	Glu	Ala	Gly	Ala	Pro	Ser	Gly	Leu	Arg	Gly	Pro	Glu
	50					55					60				
Ala	Ala	Gly	Gly	Pro	Leu	His	Leu	Leu	His	Leu	Arg	Pro	Leu	Leu	Pro
65					70					75					80
Leu	Leu	Gln	Ser	Pro	Asn	His	Pro	Pro	Ala	Gln	His	Gly	Pro	Ala	Ala
			85						90					95	
Lys	Pro	Thr	Leu	Pro	Val	Ala	Thr	Thr	Thr	Ala	Gln	Pro	Thr	Phe	Pro
			100					105					110		

Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg
 115 120 125
 His Arg Gln Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys
 130 135 140
 Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His
 145 150 155 160
 Tyr Ile Arg His Ala Arg Gly Glu Leu
 165

<210> 403

<211> 367

<212> PRT

<213> Homo sapiens

<400> 403

Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Leu Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Ala Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240
 Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
 245 250 255
 Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
 260 265 270
 Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
 275 280 285
 Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
 290 295 300
 Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
 305 310 315 320
 Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
 325 330 335
 Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly

340 345 350
 Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile
 355 360 365

<210> 404
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 404
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Pro Val Pro Val
 20

<210> 405
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
 210 215 220
 Val
 225

<210> 406
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 406

Met	Asp	Pro	Gly	Asp	Asp	Trp	Leu	Val	Glu	Ser	Leu	Arg	Leu	Tyr	Gln
1				5					10					15	
Asp	Phe	Tyr	Ala	Phe	Asp	Leu	Ser	Gly	Ala	Thr	Arg	Val	Leu	Glu	Trp
			20					25					30		
Ile	Asp	Asp	Lys	Gly	Val	Phe	Val	Ala	Gly	Tyr	Glu	Ser	Leu	Lys	Lys
			35				40						45		
Asn	Glu	Ile	Leu	His	Leu	Lys	Leu	Pro	Leu	Arg	Leu	Ser	Val	Lys	Glu
						55					60				
Asn	Lys	Gly	Leu	Phe	Pro	Glu	Arg	Asp	Phe	Lys	Val	Arg	His	Gly	Gly
65					70					75				80	
Phe	Ser	Asp	Arg	Ser	Ile	Phe	Asp	Leu	Lys	His	Val	Pro	His	Thr	Arg
				85					90					95	
Leu	Leu	Val	Thr	Ser	Gly	Leu	Pro	Gly	Cys	Tyr	Leu	Gln	Val	Trp	Gln
			100					105					110		
Val	Ala	Glu	Asp	Ser	Asp	Val	Ile	Lys	Ala	Val	Ser	Thr	Ile	Ala	Val
			115				120					125			
His	Glu	Lys	Glu	Glu	Ser	Leu	Trp	Pro	Arg	Val	Ala	Val	Phe	Ser	Thr
			130			135					140				
Leu	Ala	Pro	Gly	Val	Leu	His	Gly	Ala	Arg	Leu	Arg	Ser	Leu	Gln	Val
145					150					155					160
Val	Asp	Leu	Glu	Ser	Arg	Lys	Thr	Thr	Tyr	Thr	Ser	Asp	Val	Ser	Asp
				165					170					175	
Ser	Glu	Glu	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asp	Ala	Asp	Thr	Phe	Ala
			180					185					190		
Phe	Cys	Cys	Ala	Ser	Gly	Arg	Leu	Gly	Leu	Val	Asp	Thr	Arg	Gln	Lys
		195					200					205			
Trp	Ala	Pro	Leu	Glu	Asn	Arg	Ser	Pro	Gly	Pro	Gly	Ser	Gly	Gly	Glu
		210				215					220				
Arg	Trp	Cys	Ala	Glu	Val	Gly	Ser	Trp	Gly	Gln	Gly	Pro	Gly	Pro	Ser
225					230					235					240
Ile	Ala	Ser	Leu	Ser	Ser	Asp	Gly	Arg	Leu	Cys	Leu	Leu	Asp	Pro	Arg
				245					250					255	
Asp	Leu	Cys	His	Pro	Val	Ser	Ser	Val	Gln	Cys	Pro	Val	Ser	Val	Pro
			260					265					270		
Ser	Pro	Asp	Pro	Glu	Leu	Leu	Arg	Val	Thr	Trp	Ala	Pro	Gly	Leu	Lys
			275				280					285			
Asn	Cys	Leu	Ala	Ile	Ser	Gly	Phe	Asp	Gly	Thr	Val	Gln	Val	Tyr	Asp
		290				295					300				
Ala	Thr	Ser	Trp	Asp	Gly	Thr	Arg	Ser	Gln	Asp	Gly	Thr	Arg	Ser	Gln
305					310					315					320
Val	Glu	Pro	Leu	Phe	Thr	His	Arg	Gly	His	Ile	Phe	Leu	Asp	Gly	Asn
				325					330					335	
Gly	Met	Asp	Pro	Ala	Pro	Leu	Val	Thr	Thr	His	Thr	Trp	His	Pro	Cys
			340					345					350		
Arg	Pro	Arg	Thr	Leu	Leu	Ser	Ala	Thr	Asn	Asp	Ala	Ser	Leu	His	Val
		355					360					365			
Trp	Asp	Trp	Val	Asp	Leu	Cys	Ala	Pro	Arg						
		370				375									

<210> 407

<211> 43

<212> PRT

<213> Homo sapiens

<400> 407

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	Val
1				5					10					15	
Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	Arg	Val

20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
 35 40

<210> 408
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
 1 5 10 15
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
 20 25 30
 Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
 35 40 45
 Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
 50 55 60
 Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
 65 70 75 80
 Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
 85 90 95
 Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
 100 105 110
 Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
 115 120 125
 Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
 130 135 140
 Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
 145 150 155 160
 Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
 165 170 175
 Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
 180 185 190
 Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
 195 200 205
 Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 210 215 220
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 225 230 235 240
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 245 250 255
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 260 265 270
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 275 280 285
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 290 295 300
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 305 310 315 320
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 325 330 335
 Gly Pro Lys Lys Gly Gly Gly Ser Lys
 340 345

<210> 409
 <211> 236
 <212> PRT

<213> Homo sapiens

<400> 409

Met	Lys	Arg	Ser	Gly	Asn	Pro	Gly	Ala	Glu	Val	Thr	Asn	Ser	Ser	Val
1				5					10					15	
Ala	Gly	Pro	Asp	Cys	Cys	Gly	Gly	Leu	Gly	Asn	Ile	Asp	Phe	Arg	Gln
			20					25					30		
Ala	Asp	Phe	Cys	Val	Met	Thr	Arg	Leu	Leu	Gly	Tyr	Val	Asp	Pro	Leu
		35					40					45			
Asp	Pro	Ser	Phe	Val	Ala	Ala	Val	Ile	Thr	Ile	Thr	Phe	Asn	Pro	Leu
	50					55					60				
Tyr	Trp	Asn	Val	Val	Ala	Arg	Trp	Glu	His	Lys	Thr	Arg	Lys	Leu	Ser
65					70					75					80
Arg	Ala	Phe	Gly	Ser	Pro	Tyr	Leu	Ala	Cys	Tyr	Ser	Leu	Ser	Ile	Thr
				85					90					95	
Ile	Leu	Leu	Leu	Asn	Phe	Leu	Arg	Ser	His	Cys	Phe	Thr	Gln	Ala	Met
			100					105					110		
Leu	Ser	Gln	Pro	Arg	Met	Glu	Ser	Leu	Asp	Thr	Pro	Ala	Ala	Tyr	Ser
		115					120					125			
Leu	Val	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Val	Val	Leu	Val	Leu	Ser	Ser
	130					135					140				
Phe	Phe	Ala	Leu	Gly	Phe	Ala	Gly	Thr	Phe	Leu	Gly	Asp	Tyr	Phe	Gly
145					150					155					160
Ile	Leu	Lys	Glu	Ala	Arg	Val	Thr	Val	Phe	Pro	Phe	Asn	Ile	Leu	Asp
				165					170					175	
Asn	Pro	Met	Tyr	Trp	Gly	Ser	Thr	Ala	Asn	Tyr	Leu	Gly	Trp	Ala	Ile
			180					185					190		
Met	His	Ala	Ser	Pro	Thr	Gly	Leu	Leu	Leu	Thr	Val	Leu	Val	Ala	Leu
		195					200					205			
Thr	Tyr	Ile	Val	Ala	Leu	Leu	Tyr	Glu	Glu	Pro	Phe	Thr	Ala	Glu	Ile
	210				215						220				
Tyr	Arg	Gln	Lys	Ala	Ser	Gly	Ser	His	Lys	Arg	Ser				
225					230					235					

<210> 410

<211> 121

<212> PRT

<213> Homo sapiens

<400> 410

Met	Asn	Thr	Glu	Ala	Glu	Gln	Gln	Leu	Leu	His	His	Ala	Arg	Asn	Gly
1				5					10					15	
Asn	Ala	Glu	Glu	Val	Arg	Gln	Leu	Leu	Glu	Thr	Met	Ala	Ser	Asn	Glu
			20					25					30		
Val	Ile	Ala	Asp	Ile	Asn	Cys	Lys	Gly	Arg	Ser	Lys	Ser	Asn	Leu	Gly
		35					40					45			
Trp	Thr	Pro	Leu	His	Leu	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp
	50					55					60				
Gln	Asp	Leu	Leu	Lys	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp	Met
65					70					75					80
Gly	Asp	Thr	Pro	Leu	His	Arg	Ala	Ala	Phe	Thr	Gly	Arg	Lys	Val	Lys
				85					90					95	
Ile	Ile	Leu	Cys	Ser	Met	Phe	Val	Ser	Glu	Val	Phe	Gly	Gly	Val	Val
			100					105					110		
Thr	Ile	Val	Phe	Ser	Val	Ile	Thr	Ile							
	115						120								

<210> 411

<211> 170
 <212> PRT
 <213> Homo sapiens

<400> 411

Met	Arg	Leu	Gln	Gly	Ala	Ile	Phe	Val	Leu	Leu	Pro	His	Leu	Gly	Pro
1			5						10					15	
Ile	Leu	Val	Trp	Leu	Phe	Thr	Arg	Asp	His	Met	Ser	Gly	Trp	Cys	Glu
		20					25						30		
Gly	Pro	Arg	Met	Leu	Ser	Trp	Cys	Pro	Phe	Tyr	Lys	Val	Leu	Leu	Leu
		35					40					45			
Val	Gln	Thr	Ala	Ile	Tyr	Ser	Val	Val	Gly	Tyr	Ala	Ser	Tyr	Leu	Val
	50					55					60				
Trp	Lys	Asp	Leu	Gly	Gly	Gly	Leu	Gly	Trp	Pro	Leu	Ala	Leu	Pro	Leu
65				70						75				80	
Gly	Leu	Tyr	Ala	Val	Gln	Leu	Thr	Ile	Ser	Trp	Thr	Val	Leu	Val	Leu
			85					90					95		
Phe	Phe	Thr	Val	His	Asn	Pro	Gly	Leu	Ala	Leu	Leu	His	Leu	Leu	Leu
			100					105					110		
Leu	Tyr	Gly	Leu	Val	Val	Ser	Thr	Ala	Leu	Ile	Trp	His	Pro	Ile	Asn
		115					120					125			
Lys	Leu	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Tyr	Leu	Ala	Trp	Leu	Thr	Val
	130					135					140				
Thr	Ser	Ala	Leu	Thr	Tyr	His	Leu	Trp	Arg	Asp	Ser	Leu	Cys	Pro	Val
145					150					155					160
His	Gln	Pro	Gln	Pro	Thr	Glu	Lys	Ser	Asp						
			165						170						

<210> 412
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 412

Met	Leu	Ser	Lys	Gly	Leu	Lys	Arg	Lys	Arg	Glu	Glu	Glu	Glu	Glu	Lys
1				5					10					15	
Glu	Pro	Leu	Ala	Val	Asp	Ser	Trp	Trp	Leu	Asp	Pro	Gly	His	Thr	Ala
		20					25						30		
Val	Ala	Gln	Ala	Pro	Pro	Ala	Val	Ala	Ser	Ser	Ser	Leu	Phe	Asp	Leu
		35					40					45			
Ser	Val	Leu	Lys	Leu	His	His	Ser	Leu	Gln	Gln	Ser	Glu	Pro	Asp	Leu
	50					55					60				
Arg	His	Leu	Val	Leu	Val	Val	Asn	Thr	Leu	Arg	Arg	Ile	Gln	Ala	Ser
65				70						75				80	
Met	Ala	Pro	Ala	Ala	Ala	Leu	Pro	Pro	Val	Pro	Ser	Pro	Pro	Ala	Ala
			85						90					95	
Pro	Ser	Val	Ala	Asp	Asn	Leu	Leu	Ala	Ser	Ser	Asp	Ala	Ala	Leu	Ser
		100						105					110		
Ala	Ser	Met	Ala	Ser	Leu	Leu	Glu	Asp	Leu	Ser	His	Ile	Glu	Gly	Leu
		115					120					125			
Ser	Gln	Ala	Pro	Gln	Pro	Leu	Ala	Asp	Glu	Gly	Pro	Pro	Gly	Arg	Ser
	130					135					140				
Ile	Gly	Gly	Ala	Ala	Pro	Ser	Leu	Gly	Ala	Leu	Asp	Leu	Leu	Gly	Pro
145					150					155					160
Ala	Thr	Gly	Cys	Leu	Leu	Asp	Asp	Gly	Leu	Glu	Gly	Leu	Phe	Glu	Asp
			165						170					175	
Ile	Asp	Thr	Ser	Met	Tyr	Asp	Asn	Glu	Leu	Trp	Ala	Pro	Ala	Ser	Glu
			180					185						190	

Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
 195 200 205
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly
 210 215 220
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
 225 230 235

<210> 413
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 413
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe
 20 25 30
 Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr Lys
 35 40 45
 Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly Arg
 50 55 60
 Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe Phe
 65 70 75 80
 Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu Asp
 85 90 95
 Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val His
 100 105 110
 Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg Asp
 115 120 125
 Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser Pro
 130 135 140
 Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr Ile
 145 150 155 160
 Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln Gln His
 165 170 175
 Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu Pro
 180 185 190

<210> 414
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln Ala Gly Lys
 1 5 10 15
 Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly Gly Ala Ala
 20 25 30
 Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe Ser Gln Thr
 35 40 45
 Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu Leu Thr Leu
 50 55 60
 Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg Arg Val Ile
 65 70 75 80
 Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile Pro Asp Phe
 85 90 95
 Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys Tyr His Leu
 100 105 110

Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys His Pro
115 120 125
Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln Phe Lys
130 135 140
Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu
145 150 155 160
Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala
165 170 175
Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr
180 185 190
Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp
195 200 205
Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys
210 215 220
Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro
225 230 235 240
Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu
245 250 255
Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu
260 265 270
Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu
275 280 285
Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly
290 295 300
Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp
305 310 315 320
Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly
325 330 335
Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile
340 345 350
Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser
355 360 365
Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu
370 375 380
Arg Glu Lys Pro Gln
385

<210> 415

<211> 481

<212> PRT

<213> Homo sapiens

<400> 415

Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp
1 5 10 15
Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln
20 25 30
Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu
35 40 45
Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp
50 55 60
Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln
65 70 75 80
Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys
85 90 95
Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala
100 105 110
Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg

Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro
50						55					60				
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln
65					70					75					80
Val	Leu	Val	Val	Gly	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala
				85					90					95	
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr
			100					105					110		
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met
		115					120					125			
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln
		130				135					140				
Val	Arg	Val	Tyr	Glu	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser
145					150					155					160
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys
				165					170					175	
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe
			180					185					190		
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu
		195				200						205			
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val
		210				215					220				
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser
225					230					235					240
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly
				245					250					255	
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala
			260					265					270		
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly
		275					280					285			
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu
		290				295					300				
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys
305					310					315					320
Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly
				325				330						335	
Val	Ala	Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp
			340					345					350		

<210> 417

<211> 20

<212> PRT

<213> Homo sapiens

<400> 417

Met	Lys	Gly	Leu	Tyr	Phe	Gln	Gln	Ser	Ser	Thr	Asp	Glu	Glu	Ile	Thr
1				5					10					15	
Phe	Val	Phe	Gln												
			20												

<210> 418

<211> 320

<212> PRT

<213> Homo sapiens

<400> 418

Met	Lys	Gly	Leu	Tyr	Phe	Gln	Gln	Ser	Ser	Thr	Asp	Glu	Glu	Ile	Thr
1				5					10					15	
Phe	Val	Phe	Gln	Glu	Lys	Glu	Asp	Leu	Pro	Val	Thr	Glu	Asp	Asn	Phe
			20					25					30		
Val	Lys	Leu	Gln	Val	Lys	Ala	Cys	Ala	Leu	Ser	Gln	Ile	Asn	Thr	Lys
		35					40					45			
Leu	Leu	Ala	Glu	Met	Lys	Met	Lys	Lys	Asp	Leu	Phe	Pro	Val	Gly	Arg
	50					55					60				
Glu	Ile	Ala	Gly	Ile	Val	Leu	Asp	Val	Gly	Ser	Lys	Val	Ser	Phe	Phe
65					70					75					80
Gln	Pro	Asp	Asp	Glu	Val	Val	Gly	Ile	Leu	Pro	Leu	Asp	Ser	Glu	Asp
			85						90					95	
Pro	Gly	Leu	Cys	Glu	Val	Val	Arg	Val	His	Glu	His	Tyr	Leu	Val	His
			100					105					110		
Lys	Pro	Glu	Lys	Val	Thr	Trp	Thr	Glu	Ala	Ala	Gly	Ser	Ile	Arg	Asp
		115					120					125			
Gly	Val	Arg	Ala	Tyr	Thr	Ala	Leu	His	Tyr	Leu	Ser	His	Leu	Ser	Pro
	130					135					140				
Gly	Lys	Ser	Val	Leu	Ile	Met	Asp	Gly	Ala	Ser	Ala	Phe	Gly	Thr	Ile
145					150					155					160
Ala	Ile	Gln	Leu	Ala	His	His	Arg	Gly	Ala	Lys	Val	Ile	Ser	Thr	Ala
				165					170					175	
Cys	Ser	Leu	Glu	Asp	Lys	Gln	Cys	Leu	Glu	Arg	Phe	Arg	Pro	Pro	Ile
		180						185					190		
Ala	Arg	Val	Ile	Asp	Val	Ser	Asn	Gly	Lys	Val	His	Val	Ala	Glu	Ser
		195					200					205			
Cys	Leu	Glu	Glu	Thr	Gly	Gly	Leu	Gly	Val	Asp	Ile	Val	Leu	Asp	Ala
	210					215					220				
Gly	Val	Arg	Leu	Tyr	Ser	Lys	Asp	Asp	Glu	Pro	Ala	Val	Lys	Leu	Gln
225					230					235					240
Leu	Leu	Pro	His	Lys	His	Asp	Ile	Ile	Thr	Leu	Leu	Gly	Val	Gly	Gly
			245						250					255	
His	Trp	Val	Thr	Thr	Glu	Glu	Asn	Leu	Gln	Leu	Asp	Pro	Pro	Asp	Ser
		260						265					270		
His	Cys	Leu	Phe	Leu	Lys	Gly	Ala	Thr	Leu	Ala	Phe	Leu	Asn	Asp	Glu
		275					280					285			
Val	Trp	Asn	Leu	Ser	Asn	Val	Gln	Gln	Gly	Lys	Tyr	Leu	Tyr	Leu	Lys
	290					295					300				
Gly	Cys	Asp	Gly	Glu	Val	Ile	Asn	Trp	Cys	Phe	Gln	Thr	Ser	Val	Gly
305					310					315					320

<210> 419
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 419

Met	Glu	Lys	Leu	Arg	Arg	Val	Leu	Ser	Gly	Gln	Asp	Asp	Glu	Glu	Gln
1			5						10					15	
Gly	Leu	Thr	Ala	Gln	Val	Leu	Asp	Ala	Ser	Ser	Leu	Ser	Phe	Asn	Thr
			20					25					30		
Arg	Leu	Lys	Trp	Phe	Ala	Ile	Cys	Phe	Val	Cys	Gly	Val	Phe	Phe	Ser
		35					40					45			
Ile	Leu	Gly	Thr	Gly	Leu	Leu	Trp	Leu	Pro	Gly	Gly	Ile	Lys	Leu	Phe
	50					55					60				
Ala	Val	Phe	Tyr	Thr	Leu	Gly	Asn	Leu	Ala	Ala	Leu	Ala	Ser	Thr	Cys
65					70					75					80
Phe	Leu	Met	Gly	Pro	Val	Lys	Gln	Leu	Lys	Lys	Met	Phe	Glu	Ala	Thr

				85				90					95				
Arg	Leu	Leu	Ala	Thr	Ile	Val	Met	Leu	Leu	Cys	Phe	Ile	Phe	Thr	Leu		
			100					105					110				
Cys	Ala	Ala	Leu	Trp	Trp	His	Lys	Lys	Gly	Leu	Ala	Val	Leu	Phe	Cys		
		115					120					125					
Ile	Leu	Gln	Phe	Leu	Ser	Met	Thr	Trp	Tyr	Ser	Leu	Ser	Tyr	Ile	Pro		
	130					135					140						
Tyr	Ala	Arg	Asp	Ala	Val	Ile	Lys	Cys	Cys	Ser	Ser	Leu	Leu	Ser			
145					150					155							

<210> 420

<211> 183

<212> PRT

<213> Homo sapiens

<400> 420

Met	Glu	Gln	Arg	Leu	Ala	Glu	Phe	Arg	Ala	Ala	Arg	Lys	Arg	Ala	Gly		
1			5					10				15					
Leu	Ala	Ala	Gln	Pro	Pro	Ala	Ala	Ser	Gln	Gly	Ala	Gln	Thr	Pro	Gly		
		20						25				30					
Glu	Lys	Ala	Glu	Ala	Ala	Ala	Thr	Leu	Lys	Ala	Ala	Pro	Gly	Trp	Leu		
	35						40					45					
Lys	Arg	Phe	Leu	Val	Trp	Lys	Pro	Arg	Pro	Ala	Ser	Ala	Arg	Ala	Gln		
	50					55					60						
Pro	Gly	Leu	Val	Gln	Glu	Ala	Ala	Gln	Pro	Gln	Gly	Ser	Thr	Ser	Glu		
65				70						75					80		
Thr	Pro	Trp	Asn	Thr	Ala	Ile	Pro	Leu	Pro	Ser	Cys	Trp	Asp	Gln	Ser		
			85					90						95			
Phe	Leu	Thr	Asn	Ile	Thr	Phe	Leu	Lys	Val	Leu	Leu	Trp	Leu	Val	Leu		
			100					105					110				
Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu	Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu		
	115						120					125					
Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val	Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys		
	130					135					140						
Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr	Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu		
145				150						155				160			
Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala	Glu	Gln	Leu	Glu	Arg	Glu	Leu	Gln		
			165					170						175			
Leu	Arg	Pro	Leu	Ala	Gly	Arg											
			180														

<210> 421

<211> 143

<212> PRT

<213> Homo sapiens

<400> 421

Met	Ala	Ala	Pro	Arg	Arg	Gly	Arg	Gly	Ser	Ser	Thr	Val	Leu	Ser	Ser		
1			5					10					15				
Val	Pro	Leu	Gln	Met	Leu	Phe	Tyr	Leu	Ser	Gly	Thr	Tyr	Tyr	Ala	Leu		
		20						25				30					
Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Met	Ile	Thr	Tyr	Lys	Ser	Gln	Val	Phe		
	35						40					45					
Ser	Tyr	Pro	His	Arg	Tyr	Leu	Val	Leu	Asp	Leu	Ala	Leu	Leu	Phe	Leu		
	50					55					60						
Met	Gly	Ile	Leu	Glu	Ala	Val	Arg	Leu	Tyr	Leu	Gly	Thr	Arg	Gly	Asn		
65				70						75					80		
Leu	Thr	Glu	Ala	Glu	Arg	Pro	Leu	Ala	Ala	Ser	Leu	Ala	Leu	Thr	Ala		

85 90 95
 Gly Thr Ala Leu Leu Ser Ala His Phe Leu Leu Trp Gln Ala Leu Val
 100 105 110
 Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly
 115 120 125
 Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg
 130 135 140

<210> 422
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 422
 Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu
 1 5 10 15
 Pro Val Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val
 20 25 30
 Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala
 35 40 45
 Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu
 50 55 60
 His Lys Phe His Gly Gln Val Gln Phe
 65 70

<210> 423
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser
 1 5 10 15
 Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn
 20 25 30
 Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His
 35 40 45
 His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser
 50 55 60
 Ser Leu Leu Cys Arg Pro Leu Gln Leu Ser Phe Leu Val Ile Gln Ser
 65 70 75 80
 Val Arg Met Arg Ala Cys Gly Cys Asp Ser Gly His Cys Arg Ile Leu
 85 90 95
 Gly Arg Tyr Ser Leu Leu Gly Trp Ser Gln Gly His Arg Ala Arg Gly
 100 105 110
 Arg Gly Gly Val Ser Leu Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser
 115 120 125
 Glu Gly Gln Gly Gln Trp Leu Met Pro Val Ile Pro Ala Phe
 130 135 140

<210> 424
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 424
 Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr Ala
 1 5 10 15

Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro
 20 25 30
 Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala
 35 40 45
 Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala Asp
 50 55 60
 Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys Pro
 65 70 75 80
 Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser Leu
 85 90 95
 Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro Glu
 100 105 110
 Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val Gln
 115 120 125
 Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser Arg
 130 135 140
 Asn Asp Glu Thr Leu
 145

<210> 425

<211> 75

<212> PRT

<213> Homo sapiens

<400> 425

Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys Asn Phe Ala Leu Ser
 1 5 10 15
 Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu Val Glu Lys His Asn
 20 25 30
 Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly Pro Ser Leu Ser Ser
 35 40 45
 Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu Ile Leu Val Ala Thr
 50 55 60
 Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
 65 70 75

<210> 426

<211> 168

<212> PRT

<213> Homo sapiens

<400> 426

Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn
 1 5 10 15
 Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser
 20 25 30
 Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln
 35 40 45
 Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser
 50 55 60
 Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp
 65 70 75 80
 Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu
 85 90 95
 Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu
 100 105 110
 Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe
 115 120 125

Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu
 130 135 140
 Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile
 145 150 155 160
 Ile Val Phe Ile Leu Ile Phe Phe
 165

<210> 427
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 427
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Asp Arg Val
 85 90 95
 Ser Pro Cys Cys Pro Gly Trp Ser Gln Thr Pro Val Ile Leu Pro Pro
 100 105 110
 Gln Pro Ser Glu Val Leu Gly Leu Gln Met Gln Ala Ala Val Pro Glu
 115 120 125
 Ala His Gly Glu Asp Arg His Ser Ala Pro Leu Cys Phe Arg Cys Val
 130 135 140
 Pro Gly Pro Cys Pro Val Pro Gly Gly Gly Ile Pro Gly Pro Trp His
 145 150 155 160

<210> 428
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 428
 Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
 1 5 10 15
 Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
 20 25 30
 Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg
 35 40 45
 Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro
 50 55 60
 Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
 65 70 75 80
 Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser
 85 90

<210> 429
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 429

Met	Lys	Ala	Ser	Gly	Pro	Asp	Leu	Ser	Asp	Gly	Leu	His	Cys	Pro	Ser
1				5					10					15	
Leu	Ile	Arg	His	Leu	Arg	Thr	Phe	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Pro
			20					25					30		
Arg	Tyr	Pro	Thr	Arg	Leu	Pro	Ser	Ser	Leu	Leu	Leu	Trp	His	Leu	Cys
		35					40					45			
Gln	Cys	Leu	His	Leu	Leu	Tyr	Ala	Val	Ser	Thr	Ser	Cys	Asn	Ser	His
	50					55					60				
Gly	Lys	Arg	Ser	Ala	Ala	Trp	Ala	Met	Thr	Arg	Thr	Glu	Asp	Thr	Asp
65					70					75					80
Ala	Leu	Thr	Asp	Ser	Phe	Asp	Asp	Ser	Phe	Ile	Ser	Ser	Ala	Asp	
			85						90					95	

<210> 430

<211> 99

<212> PRT

<213> Homo sapiens

<400> 430

Met	Lys	Lys	Lys	Glu	Glu	Thr	Thr	Leu	Ser	Glu	Met	Glu	Pro	Val	Glu
1				5					10					15	
Pro	Gln	Tyr	Gln	Leu	Val	Asn	Ala	Glu	Ser	Thr	Ser	Pro	Phe	Leu	His
			20					25					30		
Cys	Leu	Arg	Glu	Val	Ile	Gly	Glu	Tyr	Ser	Val	His	Glu	Phe	Ser	Leu
		35					40					45			
Leu	Gly	Lys	Thr	Glu	Ser	Gln	Gly	Ile	Gly	Leu	Trp	Ile	Ala	Leu	Val
	50					55					60				
Val	Phe	Leu	Ser	Phe	Leu	Ile	Phe	Ser	Thr	Ser	Phe	Tyr	Ile	Ser	Asn
65					70					75					80
Ala	Glu	Gln	Pro	Phe	Phe	Lys	Glu	Pro	Pro	Thr	Glu	Ala	Ala	Lys	Glu
			85						90					95	

Leu Ser Leu

<210> 431

<211> 122

<212> PRT

<213> Homo sapiens

<400> 431

Ile	Arg	Ala	Thr	Met	Val	Ala	Arg	Val	Trp	Ser	Leu	Met	Arg	Phe	Leu
1				5					10					15	
Ile	Lys	Gly	Ser	Val	Ala	Gly	Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln
			20					25					30		
Glu	Leu	Leu	Gly	Pro	Ser	Asp	Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala
		35					40					45			
Gly	Glu	Val	Val	Pro	Pro	Ala	Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys
	50					55					60				
Gln	Gln	Thr	Gly	Leu	Gln	Ile	Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile
65					70					75					80
Tyr	Phe	Pro	Ile	Arg	Asp	Ser	Trp	Asn	Ala	Gly	Ile	Met	Thr	Val	Met
			85						90					95	
Ser	Ala	Leu	Ser	Val	Ala	Pro	Ser	Lys	Ala	Arg	Glu	Tyr	Ser	Lys	Glu
			100					105					110		
Gly	Trp	Glu	Tyr	Val	Lys	Ala	Arg	Thr	Lys						
		115						120							

<210> 432

<211> 118
 <212> PRT
 <213> Homo sapiens

<400> 432
 Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser
 1 5 10 15
 Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys
 20 25 30
 Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr
 35 40 45
 Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln
 50 55 60
 Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp
 65 70 75 80
 Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile
 85 90 95
 Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln
 100 105 110
 Glu Arg Thr Ser Ser Leu
 115

<210> 433
 <211> 49
 <212> PRT
 <213> Homo sapiens

<400> 433
 Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
 1 5 10 15
 Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
 20 25 30
 Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
 35 40 45
 His

<210> 434
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 434
 Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val
 1 5 10 15
 Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp
 20 25 30
 Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu
 35 40 45
 Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly
 50 55 60
 Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Cys Val Trp His
 65 70 75 80
 Glu Asn Ser Gln Glu Arg Lys Tyr
 85

<210> 435
 <211> 87
 <212> PRT

Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu
50 55 60
Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser
65 70 75 80
Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys Arg Asp Ala Ser Ser Tyr
85 90 95
Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile Gly Pro Cys Gln His Gln
100 105 110

<210> 439

<211> 110

<212> PRT

<213> Homo sapiens

<400> 439

Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu Thr
1 5 10 15
Asn Ile Arg Asn Val Glu Arg Leu Lys Asp Leu Arg Ala Ser Tyr
20 25 30
Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp Leu
35 40 45
Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu Gln
50 55 60
Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro Gly
65 70 75 80
Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu Leu
85 90 95
Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly
100 105 110

<210> 440

<211> 121

<212> PRT

<213> Homo sapiens

<400> 440

Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg
1 5 10 15
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe
20 25 30
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser
35 40 45
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val
50 55 60
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly
65 70 75 80
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu
85 90 95
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly
100 105 110
Asp Lys Pro Gly Ala Asp Thr Gly Arg
115 120

<210> 441

<211> 99

<212> PRT

<213> Homo sapiens

<400> 441

Met Leu Ala Arg Ala Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val
1 5 10 15
Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr
20 25 30
His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys
35 40 45
Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala
50 55 60
Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala
65 70 75 80
Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala
85 90 95
Phe Val Asp

<210> 442

<211> 183

<212> PRT

<213> Homo sapiens

<400> 442

Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
1 5 10 15
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20 25 30
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35 40 45
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50 55 60
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65 70 75 80
Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
85 90 95
Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
100 105 110
Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
115 120 125
Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
130 135 140
Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
145 150 155 160
Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
165 170 175
Leu Pro Lys Lys Lys Lys Lys
180

<210> 443

<211> 94

<212> PRT

<213> Homo sapiens

<400> 443

Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr
1 5 10 15
Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr
20 25 30
Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys
35 40 45

Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr
 50 55 60
 Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu
 65 70 75 80
 Gly Ser Glu Glu Leu Phe Ser Ser Val Cys Trp Arg Ser Arg
 85 90

<210> 444
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 444
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105

<210> 445
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 445
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Cys Lys Leu
 85 90 95
 Leu Cys Gln Lys Leu Met Glu Lys Thr Gly Ile Leu Leu Leu Cys Ala
 100 105 110
 Phe Gly Val Ser Gln Gly Pro Ala Gln Ser Gln Val Glu Val Ser Leu
 115 120 125
 Gly Pro Gly Thr Asp Tyr Arg Thr Leu Gly Lys Thr Leu His Cys His
 130 135 140
 Val Thr Gln Phe Pro His Leu Pro Asp Gly Cys Cys Glu Asn Tyr
 145 150 155 160
 Glu Met Lys

<210> 446
 <211> 128

<212> PRT
<213> Homo sapiens

<400> 446
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1 5 10 15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20 25 30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35 40 45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
50 55 60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65 70 75 80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
85 90 95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
100 105 110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
115 120 125

<210> 447
<211> 96
<212> PRT
<213> Homo sapiens

<400> 447
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1 5 10 15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
20 25 30
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
35 40 45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
50 55 60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65 70 75 80
Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
85 90 95

<210> 448
<211> 160
<212> PRT
<213> Homo sapiens

<220> .
<221> UNSURE
<222> 114
<223> Xaa = Glu,Val

<220>
<221> UNSURE
<222> 113
<223> Xaa = His,Gln

<220>
<221> UNSURE
<222> 115

<223> Xaa = Ile,Val

<400> 448

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile Thr
1 5 10 15
Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met Lys
20 25 30
Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg Leu
35 40 45
Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met Val
50 55 60
Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu Ser
65 70 75 80
Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys Thr
85 90 95
Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln Pro
100 105 110
Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser Val
115 120 125
Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys Ala
130 135 140
Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys Cys
145 150 155 160

<210> 449

<211> 117

<212> PRT

<213> Homo sapiens

<400> 449

Met Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp
1 5 10 15
Val Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu
20 25 30
Cys Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr
35 40 45
Trp Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu
50 55 60
Leu Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser
65 70 75 80
Val Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys
85 90 95
Lys Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu
100 105 110
Leu Gly Gly Ile Ser
115

<210> 450

<211> 335

<212> PRT

<213> Homo sapiens

<400> 450

Met Cys Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val
1 5 10 15
Leu Ala Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln
20 25 30
Asp Pro Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala

35 40 45
 Ser Lys Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala
 50 55 60
 Gln Gln Ile Gly Ser His Ile Ser Leu Asn Ile Asp Pro Ala Val
 65 70 75 80
 Lys Ala Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu
 85 90 95
 Phe Ala Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn
 100 105 110
 Val Gln Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu
 115 120 125
 Ser Leu Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser
 130 135 140
 Ala Asn Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys
 145 150 155 160
 Ser Ser Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu
 165 170 175
 Arg Ala Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu
 180 185 190
 Gln Ser Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala
 195 200 205
 Asp Gly Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr
 210 215 220
 Ala Glu Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly
 225 230 235 240
 Pro Tyr Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys
 245 250 255
 Thr Pro Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr
 260 265 270
 Ser Met Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala
 275 280 285
 Glu Asn Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu
 290 295 300
 Tyr Asn Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val
 305 310 315 320
 Leu Gln Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp
 325 330 335

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys, Asn

<400> 451

Met Cys Trp Val Ile Asn His Ala Ile Leu Pro Arg Met Arg Met His
 1 5 10 15
 Ser Lys Arg Gln Thr Ile Thr Arg His Ser Ala Ser Leu Ser Phe His
 20 25 30
 Ala Leu Pro Arg Ser Ala Phe Leu Gln Leu Cys Leu Leu Arg Gln Ile
 35 40 45
 His Gln Ile Pro Cys Leu Ser Ile Phe Ser Ser Thr Leu Arg Ala Gln
 50 55 60
 Thr His Asp Ser Gly Ile Gly Cys Thr Thr Ala Xaa Pro Gly Gly Arg

65 70
Arg Gln Glu Gln Leu Arg
85

75

80

<210> 452
<211> 93
<212> PRT
<213> Homo sapiens

<400> 452
Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys
1 5 10 15
Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg
20 25 30
Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro
35 40 45
Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu
50 55 60
His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys
65 70 75 80
Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala
85 90

<210> 453
<211> 108
<212> PRT
<213> Homo sapiens

<400> 453
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe
1 5 10 15
Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu
20 25 30
Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
35 40 45
Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
50 55 60
Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln
65 70 75 80
Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln
85 90 95
Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
100 105

<210> 454
<211> 277
<212> PRT
<213> Homo sapiens

<400> 454
Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg
1 5 10 15
Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe
20 25 30
Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys
35 40 45
Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr
50 55 60

Glu Leu Ser Pro Ser Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu
65 70 75 80
Arg Pro Glu Ile Val Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp
85 90 95
Thr Tyr Gln Val His Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser
100 105 110
Lys Ala Glu Gly His Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln
115 120 125
Ile Gln Ser Lys Asp Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr
130 135 140
Ser Met Lys Lys Val Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile
145 150 155 160
Ser Glu Lys Leu Met Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly
165 170 175
Leu Tyr Asp Ser Leu Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu
180 185 190
Gly Thr Leu Glu Pro Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe
195 200 205
Pro Leu Gly Asn Asn Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg
210 215 220
Asn Arg Gly Asp Gly Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala
225 230 235 240
Gly Ser Pro Thr Ala Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val
245 250 255
Ser Pro Ser Arg Glu Leu Glu Gln Gln Val Ser Ser Arg Ala Phe
260 265 270
Lys Val Lys Arg Ile
275

<210> 455

<211> 173

<212> PRT

<213> Homo sapiens

<400> 455

Met Leu Val Met Tyr Leu Leu Ala Ala Leu Phe Gly Tyr Leu Thr Phe
1 5 10 15
Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala Tyr Ser Lys Val Tyr
20 25 30
Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu Ala Val Leu Val Ala
35 40 45
Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro Ile Arg Thr Ser Val
50 55 60
Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser Trp Ile Arg His Phe
65 70 75 80
Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn Val Leu Val Ile Leu
85 90 95
Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile Gly Ala Ser Ser Ala
100 105 110
Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe Tyr Leu Lys Leu Val
115 120 125
Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val Gly Ala Leu Ile Phe
130 135 140
Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser Met Ala Leu Ile Ile
145 150 155 160
Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys His His
165 170

<210> 456
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 456

Met	Ser	Ala	Ser	Ala	Ala	Thr	Gly	Val	Phe	Val	Leu	Ser	Leu	Ser	Ala
1			5						10					15	
Ile	Pro	Val	Thr	Tyr	Val	Phe	Asn	His	Leu	Ala	Ala	Gln	His	Asp	Ser
		20					25					30			
Trp	Thr	Ile	Val	Gly	Val	Ala	Ala	Leu	Ile	Leu	Phe	Leu	Val	Ala	Leu
		35					40					45			
Leu	Ala	Arg	Val	Leu	Val	Lys	Arg	Lys	Pro	Pro	Arg	Asp	Pro	Leu	Phe
		50				55					60				
Tyr	Val	Tyr	Ala	Val	Phe	Gly	Phe	Thr	Ser	Val	Val	Asn	Leu	Ile	Ile
65					70					75				80	
Gly	Leu	Glu	Gln	Asp	Gly	Ile	Ile	Asp	Gly	Phe	Met	Thr	His	Tyr	Leu
			85					90						95	
Arg	Glu	Gly	Glu	Pro	Tyr	Leu	Asn	Thr	Ala	Tyr	Gly	His	Met	Ile	Cys
			100					105				110			
Tyr	Trp	Asp	Gly	Ser	Ala	His	Tyr	Leu	Met	Tyr	Leu	Val	Met	Val	Ala
		115					120					125			
Ala	Ile	Ala	Trp	Glu	Glu	Thr	Tyr	Arg	Thr	Ile	Gly	Leu	Tyr	Trp	Val
		130				135					140				
Gly	Ser	Ile	Ile	Met	Ser	Val	Val	Val	Phe	Val	Pro	Gly	Asn	Ile	Val
145				150					155					160	
Gly	Lys	Tyr	Gly	Thr	Arg	Ile	Cys	Pro	Ala	Phe	Phe	Leu	Ser	Ile	Pro
				165					170					175	
Tyr	Thr	Cys	Leu	Pro	Val	Trp	Ala	Gly	Phe	Arg	Ile	Tyr	Asn	Gln	Pro
			180					185					190		
Ser	Glu	Asn	Tyr	Asn	Tyr	Pro	Ser	Lys	Val	Ile	Gln	Glu	Ala	Gln	Ala
		195					200				205				
Lys	Asp	Leu	Leu	Arg	Arg	Pro	Phe	Asp	Leu	Met	Leu	Val	Val	Cys	Leu
		210				215					220				
Leu	Leu	Ala	Thr	Gly	Phe	Cys	Leu	Phe	Arg	Gly	Leu	Ile	Ala	Leu	Asp
225				230					235					240	
Cys	Pro	Ser	Glu	Leu	Cys	Arg	Leu	Tyr	Thr	Gln	Phe	Gln	Glu	Pro	Tyr
				245					250					255	
Leu	Lys	Asp	Pro	Ala	Ala	Tyr	Pro	Lys	Ile	Gln	Met	Leu	Ala	Tyr	Met
			260					265					270		
Phe	Tyr	Ser	Val	Pro	Tyr	Phe	Val	Thr	Ala	Leu	Tyr	Gly	Leu	Val	Val
			275				280					285			
Pro	Gly	Cys	Ser	Trp	Met	Pro	Asp	Ile	Thr	Leu	Ile	His	Ala	Gly	Gly
		290				295					300				
Leu	Ala	Gln	Ala	Gln	Phe	Ser	His	Ile	Gly	Ala	Ser	Leu	His	Ala	Arg
305					310					315					320
Thr	Ala	Tyr	Val	Tyr	Arg	Val	Pro	Glu	Glu	Ala	Lys	Ile	Leu	Phe	Leu
				325					330					335	
Ala	Leu	Asn	Ile	Ala	Tyr	Gly	Val	Leu	Pro	Gln	Leu	Leu	Ala	Tyr	Arg
			340					345					350		
Cys	Ile	Tyr	Lys	Pro	Glu	Phe	Phe	Ile	Lys	Thr	Lys	Ala	Glu	Glu	Lys
		355					360					365			
Val	Glu														
															370

<210> 457
 <211> 393
 <212> PRT

<213> Homo sapiens

<400> 457

Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu
1 5 10 15
Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly
20 25 30
Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr
35 40 45
Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr
50 55 60
Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu His
65 70 75 80
Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser
85 90 95
Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr
100 105 110
Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala
115 120 125
Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn
130 135 140
Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys
145 150 155 160
Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu
165 170 175
Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His
180 185 190
Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp
195 200 205
Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr
210 215 220
Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr
225 230 235 240
Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val
245 250 255
Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg
260 265 270
Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp
275 280 285
Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn Cys
290 295 300
Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu Ser
305 310 315 320
Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu Leu
325 330 335
Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg His
340 345 350
Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala Leu
355 360 365
Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu Pro
370 375 380
Met Glu Ser Gly Lys Glu Lys Ala Thr
385 390

<210> 458

<211> 116

<212> PRT

<213> Homo sapiens

<400> 458

Met Val Gly Gly Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly
 1 5 10 15
 Val Arg Gln Ala Ala Asp Phe Ala Glu Gln Phe Arg Ser Tyr Ser Glu
 20 25 30
 Ser Glu Lys Gln Trp Lys Ala Arg Met Glu Phe Ile Leu Arg His Leu
 35 40 45
 Pro Asp Tyr Arg Asp Pro Pro Asp Gly Ser Gly Arg Leu Asp Gln Leu
 50 55 60
 Leu Ser Leu Ser Met Val Trp Ala Asn His Leu Phe Leu Gly Cys Ser
 65 70 75 80
 Tyr Asn Lys Asp Leu Leu Asp Lys Val Met Glu Met Ala Asp Gly Ile
 85 90 95
 Glu Val Glu Asp Leu Pro Gln Phe Thr Arg Ser Glu Leu Met Lys
 100 105 110
 Lys His Gln Ser
 115

<210> 459

<211> 163

<212> PRT

<213> Homo sapiens

<400> 459

Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
 1 5 10 15
 Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
 20 25 30
 Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
 35 40 45
 Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
 50 55 60
 Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
 65 70 75 80
 Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln Thr Glu Asp Ser Trp
 85 90 95
 Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro Leu Thr Val Arg Arg
 100 105 110
 His Val Pro Ala Val Trp Val Leu Leu Ser Arg Asp Pro Leu Asp Pro
 115 120 125
 Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
 130 135 140
 Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg Arg Ala Arg Asp
 145 150 155 160
 Thr Arg Ser

<210> 460

<211> 230

<212> PRT

<213> Homo sapiens

<400> 460

Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
 1 5 10 15
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala
 20 25 30
 Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
 1 5 10 15
 Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
 20 25 30
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 35 40 45
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Ala Thr Leu
 50 55 60
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 65 70 75 80
 Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro
 85 90

<210> 463
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 463
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Lys Leu Leu Pro Leu Asp
 35 40 45
 Thr Tyr Val Glu Ser Pro Ala Ala Val Met Glu Leu Val Pro Ser Asp
 50 55 60
 Lys Glu Arg Gly Leu Gln Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile
 65 70 75 80
 Leu Arg Arg Ala Gly Cys Val Arg Ala Leu Ala Lys Ile Glu Arg Phe
 85 90 95
 Glu Phe Tyr Glu Arg Ala Lys Lys Ala Phe Ala Val Val Ala Thr Gly
 100 105 110
 Glu Thr Ala Leu Tyr Gly Asn Leu Ile Leu Arg Lys Gly Val Leu Ala
 115 120 125
 Leu Asn Pro Leu Leu
 130

<210> 464
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Ala Ala Ala Pro Gly His
 35 40 45
 Leu Cys Gly Glu Ser Gly Cys Ser His Gly Ala Gly Ala Gln Arg Gln
 50 55 60
 Gly Glu Gly Pro Ala Asp Pro Ser Val Asp Gly Val Arg Val His Pro
 65 70 75 80
 Thr Gln Gly Arg Leu Cys Glu Ser Pro Gly Lys Asp Arg Glu Val
 85 90 95

<210> 465

<211> 93
 <212> PRT
 <213> Homo sapiens

<400> 465
 Met Thr Pro Ile Lys Leu Leu Asn Leu Thr Ser Arg Tyr Asn Phe Arg
 1 5 10 15
 Arg Thr Phe Gly Ile Glu Leu Ser Ser Asn Ser Ser Tyr Cys Lys Arg
 20 25 30
 Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys Glu Cys Glu Cys Asn Trp
 35 40 45
 Leu His Leu Glu Ser Asp Thr Leu Lys Lys Leu Pro Ile Ile Ser Pro
 50 55 60
 Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu Tyr Phe Ser Gly Gln Leu
 65 70 75 80
 Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu Ile Lys Leu
 85 90

<210> 466
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 466
 Met Glu Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr
 1 5 10 15
 Val Glu Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile
 20 25 30
 Gln Asp Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe
 35 40 45
 Arg Asp Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys
 50 55 60
 Ile Gln Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu
 65 70 75 80
 Cys Lys Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu
 85 90 95
 Asp Lys Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His
 100 105 110
 Pro Gln Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro
 115 120 125
 Asp Gly Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val
 130 135 140
 Gly Gln Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe
 145 150 155 160
 Met Glu Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys
 165 170 175
 Glu Leu Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His
 180 185 190
 Lys Glu Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu
 195 200 205
 Lys Leu His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu
 210 215 220
 Leu Arg Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu
 225 230 235 240
 Ser Gln Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val Ser
 245 250 255
 Ile Gln Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys Asp
 260 265 270

Ile Thr Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala
 275 280 285
 Thr Arg Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly
 290 295 300
 Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro
 305 310 315 320
 Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu
 325 330 335
 Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys
 340 345 350
 Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu
 355 360 365
 Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val
 370 375 380
 Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile
 385 390 395 400
 Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu
 405 410 415
 Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe
 420 425 430
 Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp
 435 440 445
 Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His
 450 455 460
 Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe
 465 470 475 480
 Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile
 485 490 495
 Leu His Pro Gln
 500

<210> 467
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 467
 Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe
 1 5 10 15
 Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr
 20 25 30
 Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln
 35 40 45
 Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro
 50 55 60
 Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr
 65 70 75 80
 Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln His Ile Arg Thr Ser
 85 90 95
 Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu
 100 105 110
 Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile
 115 120 125
 Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile Cys
 130 135 140

<210> 468
 <211> 100

<212> PRT

<213> Homo sapiens

<400> 468

Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
1 5 10 15
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
20 25 30
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
35 40 45
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
50 55 60
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
65 70 75 80
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
85 90 95
Trp Trp Thr Gln
100

<210> 469

<211> 119

<212> PRT

<213> Homo sapiens

<400> 469

Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly
1 5 10 15
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro
20 25 30
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu
35 40 45
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp
50 55 60
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu
65 70 75 80
Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala
85 90 95
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys
100 105 110
Arg Asn Arg Ala Trp His Lys
115

<210> 470

<211> 140

<212> PRT

<213> Homo sapiens

<400> 470

Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu
1 5 10 15
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg
20 25 30
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr
35 40 45
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln
50 55 60
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr
65 70 75 80

Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro
85 90 95
Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr
100 105 110
Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser
115 120 125
Lys Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
130 135 140

<210> 471
<211> 109
<212> PRT
<213> Homo sapiens

<400> 471
Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala
1 5 10 15
Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg
20 25 30
Thr Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro
35 40 45
Phe Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala
50 55 60
Trp Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys
65 70 75 80
Pro Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp
85 90 95
Ser Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu
100 105

<210> 472
<211> 100
<212> PRT
<213> Homo sapiens

<400> 472
Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala
1 5 10 15
Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg
20 25 30
Thr Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro
35 40 45
Phe Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu
50 55 60
Gly Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val
65 70 75 80
Gln Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr
85 90 95
Pro Gly Phe Lys
100

<210> 473
<211> 141
<212> PRT
<213> Homo sapiens

<400> 473
Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr


```
<400> 476
Met Leu Lys Val Glu Ala Thr Gly Ser Pro Glu Glu Gly Trp Ala Gly
1          5          10          15
Gly Glu Pro Arg Thr Gly Ala Pro Ala Asn Ser Pro Ser Cys Pro Gln
          20          25          30
Glu Met Pro Leu Gln Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr
          35          40          45
Gln Gln Leu Leu Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu
          50          55          60
Asn Val Ala Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala
65          70          75          80
Ser Gly Arg Ser Pro
          85
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<400> 477
Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu
1          5          10          15
Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe
20          25          30
Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His
35          40          45
Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val
50          55          60
Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val
65          70          75          80
Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu
85          90          95
Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile
100          105          110
Leu Ala Thr Leu
115

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<400> 478

Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu
 1 5 10 15
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe
 20 25 30
 Phe Glu Tyr Leu Glu Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser
 35 40 45
 Ala Lys Ser His His Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala
 50 55 60
 Ala Pro Leu Leu Ser Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn
 65 70 75 80
 Gly Leu Gly Lys Cys His Asp Pro His Phe Thr Gly Glu Glu Thr Glu
 85 90 95
 Ala Gln Arg Gly Lys Leu Thr Thr
 100

<210> 479
 <211> 439
 <212> PRT
 <213> Homo sapiens

<400> 479
 Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln Leu
 1 5 10 15
 Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln Arg
 20 25 30
 Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr Asn
 35 40 45
 Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys
 50 55 60
 Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn Gln
 65 70 75 80
 Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro Glu
 85 90 95
 Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser Ala
 100 105 110
 His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly Ala
 115 120 125
 Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile Leu
 130 135 140
 Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile Tyr
 145 150 155 160
 Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr Ile
 165 170 175
 Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys Tyr
 180 185 190
 Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn Cys
 195 200 205
 Leu Glu Gly Thr His Glu Phe Glu Ala Ile Gly Phe Gln Lys Val
 210 215 220
 Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val Leu
 225 230 235 240
 Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys Glu
 245 250 255
 Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg Gln Arg
 260 265 270
 Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu Pro Gly
 275 280 285
 Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln Arg Leu

290 295 300
 Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys Ala Met
 305 310 315 320
 Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu
 325 330 335
 Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr
 340 345 350
 Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu
 355 360 365
 Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys
 370 375 380
 Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro
 385 390 395 400
 Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile
 405 410 415
 Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu
 420 425 430
 Ser Ala Ile Glu Lys Leu Leu
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 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu
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 Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala
 20 25 30
 Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys
 35 40 45
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly
 50 55 60
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg
 65 70 75 80
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val
 85 90 95
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn
 100 105 110
 Tyr Thr Ser Gly
 115

<210> 481
 <211> 171
 <212> PRT
 <213> Homo sapiens

<400> 481
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly
 1 5 10 15
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe
 20 25 30
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg
 35 40 45
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr
 50 55 60
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val

65					70					75					80
Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	Pro	Gly	Tyr	Tyr	His
			85						90					95	
Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	Glu	Asp	Ala	Ile	Arg
			100					105					110		
Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	Lys	Phe	Arg	Lys	Thr
		115						120					125		
Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	Val	Leu	Leu	Ala	Tyr
		130				135					140				
Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	Gly	Met	Asn	Phe	Ile
145					150					155					160
Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Glu					
				165					170						

<210> 482
 <211> 177
 <212> PRT
 <213> Homo sapiens

<400> 482

Met	Gln	Pro	Ala	Glu	Arg	Ser	Arg	Val	Pro	Arg	Ile	Asp	Pro	Tyr	Gly
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Phe	Glu	Arg	Pro	Glu	Asp	Phe	Asp	Asp	Ala	Ala	Tyr	Glu	Lys	Phe	Phe
			20					25					30		
Ser	Ser	Tyr	Leu	Val	Thr	Leu	Thr	Arg	Arg	Ala	Ile	Lys	Trp	Ser	Arg
		35					40					45			
Leu	Leu	Gln	Gly	Gly	Gly	Val	Pro	Arg	Ser	Arg	Thr	Val	Lys	Arg	Tyr
	50					55					60				
Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala	Arg	Val	Trp	Met	Val
65					70					75					80
Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	Pro	Gly	Tyr	Tyr	His
			85						90					95	
Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	Glu	Asp	Ala	Ile	Arg
			100					105					110		
Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	Lys	Phe	Arg	Lys	Thr
		115						120					125		
Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	Val	Leu	Leu	Ala	Tyr
		130				135					140				
Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	Gly	Met	Asn	Phe	Ile
145					150					155					160
Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp	Lys	Asn	Leu	Phe	Gly
				165					170					175	

Cys